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Release 2. Copyright Di	1D John F. Collins, Biocomputing Researc (c) 1993, 1994, 1995 University of Edin. stribution rights by Intelligenetics, In
MPsrch_nn n.a.	- n.a. database search, using Smith-Waterman algorithm
Run on: Tabular output no	Thu Aug 21 09:14:35 1997; MasPar time 1721.16 Seconds 1336.190 Million cell updates/sec not generated.
Title: Description: Perfect Score:	>US-08-320-157-6 (1-2094) from USO8320157.seq 2094
	1 GAGGATCTACAGGGGACAAGCAAAAAAAAAAAGGGAGATCC 2094 CTCCTAGATGTCCCCTGTTCGTTTTTTTTTTTTT
Scoring table:	TABLE default Gap 6
Nmatch STD:	Dbase 0; Query 0
Searched:	362067 segs, 549138275 bases x 2
Post-processing:	Minimum Match 0% Listing first 45 summaries
Database:	embl-new3 1:BCT 2:FUN 3:GEN1 4:GEN2 5:HTG1 6:HTG2 7:HUM 8:INV 9:ORG 10:MAM 11:VRT 12:PLN 13:PRO 14:ROD 15:SYN 16:UNC
Database:	:BCT2 20:BCT3 21:BCT4 22:BCT5 23:BCT6 :BCT9 27:BCT10 28:BCT11 29:GEN1 30:GE :HTG1 33:HTG2 34:HTG3 35:INV1 36:INV2
	:INVS 40:INV6 41:INV7 6:INV6 41:INV7 6:MAM1 47:MAM2 48:MAM :PAT1 54:PAT2 55:PAT3 :PLN2 61:PLN3 62:PLN4
	8:PIN10 69:PIN11 70:PRI1 71:PR: 4:PRI5 75:PRI6 76:PRI7 77:PRI8 81:PRI12 82:PRI13 83:PRI14 84 7:ROD3 88:ROD4 89:ROD5 90:ROD6 SYN 95:UNA 96:VRI1 97:VRI2 98
Database:	0:VRL5 101:VRL6 102:VRL7 103:VRL8 104
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Database:	1 14
Statistics:	Mean 11.818; Variance 4.529; scale 2.609

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No. Score Match Length DB ID  No. Score Match Length DB ID  1899 90.7 6478 77 HSU168 1899 90.7 6478 77 HSU168 1899 90.7 6478 77 HSU168 1899 90.1 1949 77 HSU168 1991 90.1 1949 77 HSU168 1991 90.1 1949 77 HSU168 1991 90.1 1949 77 HSU199 1992 90.1 1949 77 HSU199 1993 90.1 1989 80 MUSCRI 1992 90.1 1989 80 MUSCRI 1993 90.1 1989 80 MUSCRI 1990 90.1 1	escription Pre	Human Bak-2 gene, c Human Bak-2 gene, c Human Bak protein m	Human Bak-3 pseudogen 0.0 H.sapiens BAK mRNA fo 0.0	Human DNA sequence ** 0.0	Human DNA for apotosi 3.0	M.musculus 94kb genom 1.3	Sequence 5 from paten 1.5	Mouse brain GAD seque 2.8 00023: HTGS phase 3. 2.8	Human 18q- syndrome b 5.5	Human anonymous gene, 5.5	Sequence 13 from pate 2.2	H.sapiens CpG island 9.0	H.sapiens PHKB gene ( 9.0	M.musculus gast gene 2.2 Bacterial cytochrome 9.0	Mus musculus gastrin 2.2	human G-aipha io prot 9.0 lactoferrin {5' regio 3.4	GSTA5=glutathione S-t 3.	GSTA5=glutathione S-t 3. transcription factor 2.2	M.musculus (BALB/c) G 2.2	Woodchuck intronless 2.2	M.musculus mRNA for g 9.0	Mouse muscle creatine 9.0	D.melanogaster fsh me 2.2	Dictyostelium discoid 2.2 Human DNA sequence fr 3.4	Mouse full-length int 9.0	D.melanogaster ish me 2.3 Mus musculus qlutathi 2.3	litis elegan 9.0	fr 9.0	chromosome 16p1 9.0		PRI 19-AUG-1995  rryotes; Metazoa; Chordata; ;; Catarrhini; Hominidae; Homo.  rrs,V.C., Wu,J.J., Umansky,S.R.,  widely distributed Bcl-2 homologue 195)
No. Score Match Lengary Match Lengary Bolds	a	HSU16811 HSU16812 HSU23765	HSCEBP1	HS291J10	D88396S1	MMTSXDNA	128278	A28072 HSAC000028	HSU19554	HUMANONYMO	114734	HS76G6F HS76G6R	HSPHKB19	MMGASTGN3 SYNBCTCONS	MMU58136	S52659			MMGSTP1	MMNMYC2 HSE2F1503	MMGAD67C	MUSMCKA MMU02313	DROFSHB	DDU32174 HSL219F9B	MUSFLIAP	DROFSHA MMU15654	H	3.5	HSU9132 HSU913	ALIGNMENTS	mRNA .e cdsal euka .rimates rrimates ., Powe .by the
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ORGANISM	Homo sapiens Fukarvotae, mitochondrial enkarvotoe, Motasoa,	qa
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vortebrata; Eutheria; Primates; Catarrhini; Hominidae; Hom;
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Chittenden, T., Harrington, E.A., O'Connor, R., Flemington, C.
Lutz, R.J., Evan, G.I. and Guild, B.C.
Induction of apoptosis by the Bcl-2 homologue Bak
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                                                              /organism="Homo sapiens"
/clone_lib="Jurkat cell cDNA library
/cell_line="Jurkat cell"
/function="induction of apoptosis"
                                    Chittenden,
e, MA 02139,
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Pred. No. 0.00e+00;
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	961 gttgggccagtttgtggtacgaagattcttcaaatcatgactcccaagggtgccctttgg 	901 cctctctgggcccaggggctgtggccgtctcctccagctctctgggacctcctta	1211 TCCCACCATTCTACCTGAGGCCAGGACGTCGGGGTGTGGGGATTGGTGGGTCTATGTTC 1 1141 cccaggattcagctattctggaagatcagcacctaagagatgggactaggacctgagcc 1 11571 cccaggattcagctattctggaagatcagcaccctaagagatgggactagacctgagcc 1 1271 cCcAGGATTCAGCTATTCTGGAAGATCAGCACCCTAAGAGATGGGACTAGGACCTGAGCC 1 1201 tggtcctggccgtccctaagcatgtgtcccaggagcaggacctactaggagaggggcc 1 1111111111111111111111111111111	1451 GTTGGACTCTGAGGGTTCTGGGCTTGGGGTGGGGGTGGGGGTGGGGGGGG	

C. Kiefer, Mol. Biol., LXR Way South, Richmond, CA 94804, USA DB 77; Length 5408; .00e+00; .hes 186; Indels 33; Gaps 23; idely distributed Bcl-2 homologue cataggccacccctatcctctgagt 1920 19-AUG-1995 V.C., Wu, J.J., Umansky, S.R., otes; Metazoa; Chordata; Satarrhini; Hominidae; Homo. n genomic DNA" PRI cds. 11 t

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2847 1381 1441 1441 2965 1501 1501 1501 1621 1621 1621 1631 1631 1632 1633 1633	LOCUS  HSCEBPI 1360 bp RNA PRI 05-MAY-1995  BEFINITION H.Sapiens BAK MRNA for BCI-2 homologue.  NID 9604984  KEYWORDS  SOURCE ORGANISM HOMO sapiens.  NEFERRENCE ORGANISM HOMO sapiens.  NEFERRENCE ORGANISM HOMO sapiens.  NEFERRENCE ORGANISM HOMO sapiens.  NEFERRENCE ORGANISM HOMO Sapiens.  NATHORS  ELVATYORISM HOMO Sapiens.  NATHORS  AUTHORS  AUTHORS  Cloning of a bci-2 homologue by interaction with adenovirus E1B 19K  NELL NATHURE 1995 Jun 1;375(6530):431]]  AUTHORS  TITLE JOURNAL NEEFERRENCE  Closes 1 to 1360)  AUTHORS  TITLE JOURNAL  AUTHORS  TITLE JOURNAL SLOWGE  Closes 1 to 1360)  AUTHORS  TITLE JOURNAL SLOWGE  Closes 1 to 1360)  AUTHORS  TITLE JOURNAL JOURNAL SLOWGE  Closes 1 to 1360)  AUTHORS  TITLE JOURNAL JOURNAL JOURNAL Greenford (25-JAN-1995) R. Brown, Glaxo Research & Development, Greenford Scad Greenford Middlesex UB6 OHE, UK  FEATURES  SOURCE  1.1360
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Order of segments is not known; 800 n's separate segments.

Onfinished sequence: dJ291.10 Contig_ID: 01371 Length: 3951 bp Unfinished sequence: dJ291.10 Contig_ID: 01622 Length: 1040 bp Unfinished sequence: dJ291.10 Contig_ID: 01422 Length: 1722 bp Unfinished sequence: dJ291.10 Contig_ID: 01057 Length: 26804 bp Unfinished sequence: dJ291.10 Contig_ID: 01537 Length: 1598 bp Unfinished sequence: dJ291.10 Contig_ID: 01231 Length: 1547 bp
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                                                                                                                                                                                                                                                                                Length 1360
                                                                                                                                                                                                                                                                                                                     17; Indels
                                     B-cell"
                                                                                                                                                                                                                                                                              Score 1274; DB 73;
Pred. No. 0.00e+00;
0; Mismatches 17;
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/clone_lib="EBV-transformed
193..828
 sapiens"
/organism="Homo
                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 98.2%;
Matches 1333; Conservative
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ORIGIN
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Submitted (14-OCT-1996) to the DDBJ/EMBL/GenBank databases. Submitted (14-OCT-1996) to the DDBJ/EMBL/GenBank databases. Hidetaka Eguchi, Saitama Cancer Center Research Institute, Depertment of Blochemistry; 818 Komuro, Ina, Kita-adachi-gun, Saitama 362, Japan (E-mail:hide4saitama-cc.go.jp, 1el:048-722-1111(ex.255), Fax:048-722-1739)
2 (bases 1 to 444)
Eguchi, H. and Hayashi, S. Estrogen alters expression of apoptosis-regulators, Bcl-2, Bcl-xL and Bak, as well as susceptibility to therapeutic agents of human Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                            D88396S2 444 bp DNA PRI 10-JAN-1997
Human DNA for apotosis-regulator Bak, exon 2, 3 and partial cds.
D88397
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     1977 AGTICTIGATICAGCCAAATGCAGGAGGGAGGCAGGCAGATG-GAGCCCATAGGCCACCCC
                                          otcagttetetecetteetetetetetatagacaettgeteeeaeceatteaetagg
                                                                  1561 CTCAGTTCTCTCCCTTCCTCTCTTATAGACACTTGCTCCCAACCCATTCACTAGGG
                                                                                                                                                                                            catctggagggttctaagtgggagaaggactatcaacaccactaggaatcccagaggtgg
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; E
                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/clone="pgEmBak01-02"
join(D88396:26.90,51.231,358.>444)
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/product="Bak"
/db_xref="PID:g1655494"
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DEFINITION
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AUTHORS
TITLE
JOURNAL
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                968
                                                                                                                                       /organism="Homo sapiens"
/clone="291J10"
/bromosome="6"
BP; 28765 A; 27932 C; 27951 G; 27528 T; 11403 other;
                                                                                                                                                                                                                                Gaps
  2194 bp
4250 bp
4036 bp
7484 bp
14415 bp
9377 bp
6493 bp
21107 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              969 GGAGG -- CCCIGCGIGGGGGCCAGICA - GGCIGCAGAGGCACCICAACAIIGCAIGGIGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 123579;
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               Length:
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   01408
00133
01390
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01327
01441
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Pred. No. 0.00e+00;
0; Mismatches 1;
  Contig_ID:
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Unfinished sequence: dJ291J10 Cd Unfinished sequence:
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Best Local Similarity 98.84;
Matches 1345; Conservative
                                                                                                                           1..123579
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/db_xref="PID: 2258462"
/db_xref="PID: 91673441"
/db_xref="PID: 91673441"
/translation="MSEKQSFKTSEAECSAMDLPEFEDEENWLFKVLGFQPGFSSALD
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KVITGNIKASPSMYMEMFTDQNPQADQDLEETESDGAMNPTD"
/47792..46119
                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 94459)
Simmler,M.C., Cunningham,D.B., Clerc,P., Vermat,T., Caudron,D.,
Cruaud,C., Pawlak,A., Szpirer,C., Weissenbach,J., Claverie,J.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                 A 94kb genomic sequence 3' to the murine Xist gene reveals an AT rich region containing a new testis specific gene Tsx Hun. Mol. Genet. In press
2 (bases 1 to 94459)
Claverie, J.
Direct Submission
Direct Submission
Submitted (06-AUG-1996) J. Claverie, Information Genetique & Structurale, CNRS EP 91, 31 Chemin Joseph Aiguier, 13402 Marseille Cedex 20, FRANCE
This gene constitutes one of the only well verified examples of a case where the AG-GT rule in not obeyed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     join(44627..44791,46180..46215,46896..46932,48355..48436,
50663..50763,52149..52207,54425..54741)
/gene-"Tsx"
44627..44791
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50663..50763,52149..52207,54425..54450)
/gene="Tsx"
           ö
                                                                                                                                                                                                                                                                                                                      Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                          15-NOV-1996
             Gaps
             ö
                                                                                                                                                                                                                       encoding Tsx gene.
             Indels
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             Mismatches
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/organism="Mus_musculus"
                                                                                                                                                                                            MMTSXDNA 94459 bp DNA
M.musculus 94kb genomic sequence
X99946
                                                                                                     /clone_lib="YAC pa-2"
/map="D-E mu"
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46180..46215
/gene="Tsx"
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46933..48354
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/number=3
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/gene="Tsx"
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             Conservative
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/translation="MLQHLQPTAENAYEYFTKIATSLFESGINWGRVVALLGFGYRLA
LHYYQHGLTGFLGGVTRFVVDFMLHHCIARWIAQRGGWVAALNLGNGPILNVLVVLGV
VLLGQFVVR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Estrogen alters expression of apoptosis-regulators, Bcl-2, Bcl-xL and Bak, as well as susceptibility to therapeutic agents of human breast cancer cells
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                                                                                                                                                                                                                                                                                                                        162 gacccgcttcgtggtcgacttcatgctgcatcactgcattgcccggtggattgcacagag 221
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                                                                                                                                                                                                                                                                                                                                                                      102 cggctaccgtctggccctacacgtctaccagcatggcctgactggcttcctaggccaggt 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (14-007-1996) to the DDBJ/EWBL/GenBank databases. Hidetaka Eguchi, Saitama Cancer Center Research Institute, Depertment of Blochemistry; 818 Komuro, Ina, Kita-adachi-gun, Saitama 362, Japan (E-mail:hide@saitama-cc.go.jp, Tel:048-722-1111(ex.255), Fax:048-722-1739)

Eguchi, H. and Hayashi, S.
                                                                                                                                                                                                                                                                         Gaps
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Eguchi, H.
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Pred. No. 7.63e-161;
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Pred. No. 3.06e-58;
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Homo sapiens
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Best Local Similarity 100.0%;
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Best Local Similarity 99.0%;
Matches 191; Conservative
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/number=2
232..357
/number=2
358..444
/number=3
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Bennett,A., Labavitch,J.M., Powell,A. and Stotz,H.
Plant inhibitors of fungal polygalacturonases and their use tentrol fungal disease
Patent: US 5569830-A 5 29-OCT-1996,
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Pred. No. 2.15e-10;
67; Mismatches 64; Indels
                                                                                                                                                                                                                                                                 Score 49; DB 86; Length 9445
Pred. No. 1.33e-19;
0; Mismatches 52; Indels
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Sequence 5 from patent US 5569830.
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50663..50763
/gene="Tsx"
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50764..52148
/gene="Tsx"
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52149..52207
/gene="Tsx"
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/gene="Tsx"
                             48437..50662
/gene="Tsx"
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Best Local Similarity 67.7%;
Matches 113; Conservative
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Best Local Similarity 16.9%;
Matches 27; Conservative
                    'number-4
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
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1 (bases 1 to 215)
Bennett,A., Labavitch,J.M., Powell,A. and Stotz,H.
Plant inhibitors of fungal polygalacturonases and their use to control fungal disease
Patent: US 5569830-A 5 29-ocr-1996;
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PACENT: WO 9214485-A 11 03-SEP-1992;
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/db_xref="PID:e204340"
/db_xref="PID:91247777"
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LPAKNGEEQTAQFLLEVVDILLNYVRKTFDRSTKVLDFHHPHQLLEGMEGFNLELSDH
PESLEQILVDCRDTLKKCWFTGHPFFRQLSTGLDIIGLAGFHLTSTANTNMFTYEIA
PVYLMEQILYDCRDTLKKWRKIVGWSNKDGDGIFSPGGAISNNYSTMARYKYFPEVKTKGMA
AVPKLVLFTSEHSHYSTKRARALGFGTDNYILIKCNERGKIIPADAGG
YVPLYVNATAGTTVYGARDPIOEIADICEKYNLMLHVDAAWGGGLLMSRKHRHKLSGI
ERANSYTWNPHKMMGVLLQCSAILVKEKGILQGCNQMCAGYLFQPDKQYDVSYDTGDK
                                                                                                                                  AIQCGRHVDIFKFWLMWKAKGTVGFENQINKCLELADYLYAKIKNREEFEMVFDGEPE
HTNVCFWYIPQSLRGVPDSPERREKLHRVAPKIKALMMESGTTMVGYQPQGDKANFFR
MVISNPAATQSDIDPLIEEIERLGQDL"
translation="MASSTPSPATSSNAGADPNTTNLRPTTYDTWCGVAHGCTRKLGI"
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Submitted (21-OCT-1996) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
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Human 18q- syndrome breakpoint satellite III DNA recombination
sequence.
U19554
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Wang, Z. and Roe, B.A. completed clone 6e4 from human chromosome 12, 45976 bp Unpublished (1996)
Weltzer, P.
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Pred. No. 2.81e-02;
0; Mismatches 9; Indels
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12130 c 12219 g 10524 t
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3 (bases 1 to 45976)
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Best Local Similarity 80.0%;
Matches 36; Conservative
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Best Local Similarity 71.4%;
Matches 45; Conservative
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Homo sapiens
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 257) Schneider, S., Trask, B.J., Overhauser, J. and Silverman, G.A. An 18q- syndrome breakpoint is located in a cluster of serpin genes and was formed by an illegitimate recombination with satellite III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryotze; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2754)
Xie, Y.G., Han, F.Y., Peyrard, M., Ruttledge, M.H., Fransson, I.,
DeJong, P., Collins, J., Pounam, I., Nordenskjold, M. and Dumanski, J.P.
Cloning of a novel, anonymous gene from a megabase-range YAC and
cosmid contig in the neurofibromatosis type 2/meningioma region on
human chromosome 22q12
Hum. Mol. Genet. 2 (9), 1361-1368 (1993)
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/translation="MSSESSKRRFWVIRSDGAPAEGKRNRSDTEQEGKYYSEEAEVD
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RLAHIRLKKGRDQTHEAKOKVDAYHLOLONLLYEVMHLOKEIIKCLEFKSKHEEIDLV
SLEEFYKEAPPDISKAEVTMGDPHQOTLARLDWELEORKRLAEKYRECLSNKEKILKE
                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (06-JAN-1995) Gary A. Silverman, Pediatrics, Harvard
Medical School, Joint Program in Neonatology, 300 Longwood Avenue
Enders-9, Boston, MA 02115, USA
Location/Qualifiers
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/isolate="JL184. an 18q syndrome patient"
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Pred. No. 5.52e-01;
0; Mismatches 17; Indels
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/tissue_lib="Stratagene #936206"
/map="22q12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="unknown filler sequence"
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27 c 90 g 63 t
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1..2754
/organism="Homo sapiens"
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80..256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /chromosome="18"
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L18972
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Best Local Similarity 71.2%;
Matches 42; Conservative
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Silverman, G.A.
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IEVKKEYLSSLOPRLNSIMQASIPVQEYLFMPFDQAHKQYETARHLPPPLYVLFVQAT
AYGQACDKTLGYAIEGSYDEAKALFKPPEDSQDDESDSDAEEEGTTKRRRPTLGVQLD
BYGKREMLKFHLSYMLDGAKCNDOSYLHGTFYTUMNINTHYKKNYTFAMELITPISAG
DLLSPDSVLSCLYFQDHGKKTPNPANOYQFDKYGIITLSDYYLELGHPYLWYQKLGGI
HFPKEQPQQTVIADHSLSASHMETTMKLLKTRVQSRLALHKQPASLEHGIVPYTSDCQ
YLFPAKVYSRLVKWYTAHEDYMELHFTKDIYDAGLAGDTNLYMALIERGTAKLQAA
VVLNPGYSSIPPIFQLCLNWKGEKTNSNDDNIRAMGEVNVYKELCGPWPSHGLTH
QLQRLCYLLDYTETESHDDSVEGPKEFPQEKMCIRLFRGPSRMKPFKYNHPQGFFSH
R*
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593 t 723 g 694 c 744 BASE COUNT ORIGIN

ö Gaps ; 0 Score 25; DB 79; Length 2754; Pred. No. 5.52e-01; 0; Mismatches 22; Indels ( 0.2%; Bost Local Similarity 68.1%; Matches 47; Conservative ç 요

289 agaacggag 297 ||| |||| 1578 GGAAGGGAG 1570 g g

Search completed: Thu Aug 21 10:27:37 1997 Job time: 4382 secs.

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch\_nn

MasPar time 218.06 Seconds 944.863 Million cell updates/sec Thu Aug 21 10:27:57 1997; Run on:

Tabular output not generated.

>US-08-320-157-6 (1-2094) from US08320157.seq 2094 Description: Perfect Score:

1 GAGGATCTACAGGGGACAAG.........CAAAAAAAAAGGGAGATCC 2094 CTCCTAGATGTCCCCTGTTC......GTTTTTTTTTTTGCCTCTAGG Sequence: N.A.

TABLE default Scoring table:

Gap

134151 seqs, 49196315 bases x 2 Searched:

Dbase 0; Query 0

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STD

Nmatch

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

iparti 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part27 25:part25 26:part26 27:part27 n-geneseq27

Mean 9.693; Variance 5.444; scale 1.780 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	-	å Query Match Length DB	DB	QI ,	Description	Pred. No.
1	2094	100.0	2094	24	T42138	Bak gene.	0.00e+00
7	2072	98.9	2072	14	095492	Human Cdn-1 cDNA.	0.00e+00
m	1899	90.7	6511	14	095493		0.00e+00
4	1886	90.1	1968	19	T17375	CDNA.	0.00e+00
'n	1496	71.4	5408	14	095494		0.00e+00
φ	883	42.2	1286	24	T42139	Bak-2 dene.	0.00e+00
c 2	95	4.5	1047	~	010572		4.06e-46
æ	1 78	3.7	1047	~	010572	Human Natriuretic Pep	2.35e-34
6	43	2.1	91	σ	051746	Oligonucleotide probe	1.89e-11
10	1 44	2.1	204	~1	N81164	Base substituted E.co	4.60e-12
c 11	45	2.1	204	1	N81164	Base substituted E.co	1.11e-12
c 12	42	2.0	91	δ	051746	Oligonucleotide probe	7.69e-11
c 13	37	1.8	114	12	070465	Generic DNA sequence	7.46e-08
c 14	36	1.7	114	12	070468	Generic DNA sequence	2.86e-07
15	34	1.6	114	12	070466	Generic DNA sequence	4.05e-06
16	34	1.6	114	12	070465	Generic DNA sequence	4.05e-06

444	4.05e- 4.05e-	1.49e-	1.95e-	5.44e-	2.38e-	6.87e-	2.38e-	8.11e-	2.71e-	2.71e-	8.86e-	8.86e-	2.83e-	2.83e-	2.83e-	2.83e-	.86e-	.86e-	.83e-	.69e+	.85e-	.85e-	.85e-	.85e-	-
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## ALIGNMENTS

Human; Bak; apoptosis; latency; virus replication;
Bstein-Barr virus; BHRRI; fusion protein; epitope tag;
drug screening; co-precipitation; ELISA; immunoassay; antibody;
protein interactive trapping; virucide; antitumour; diagnostic; ss. BP. T 1 T42138 standard; cDNA; 2094 T42138; 22-FEB-1997 (first entry) Bak gene RESULT 

Location/Qualifiers 1..200 /\*tag= b /product= Bak protein 3'UTR 837..2094 201..836 /\*tag= Key 5'UTR CDS

Homo sapiens.

24-OCT-1996: 19-APR-1996; UO5639. 20-APR-1995; US-426529. (LARB-) LAR BIOTECHNOLOGY INC. BALT PJ, Kiefer MC; WPI; 96-485886/48. /\*tag= c WO9633416-A1.

P-PSDB; W03668.

Screening for anti-viral agents - by detecting the ability of agent to disrupt the interaction of a Bak protein and a viral protein

an

Disclosure: Fig 1; 24pp; English.

The sequence encodes Bak protein, which is a bcl-1 homologue which interacts with Epstein-Barr virus (EBV) early lytic cycle BHRF1 protein, and is capable of modulating apoptosis. The Bak gene is located on human chromosome-6 at 6p21-23. The protein may be used in complete or partial form, or as an epitope tag fusion protein, in a new virucide drug screening method, which involves combination of Bak protein and a viral protein (e.g. EBV BHRF1), exposure to a test compound, and monitoring for disruption of the interaction, e.g. by co-precipitation, protein interactive trapping or ELISA. Interaction of Bak and viral proteins allows viral replication or

	latency in the absence of apoptosis. Compounds which inhibit the interaction may be used as virucide, antitumour or diagnostic agents. Sequence 2094 BP: 410 A; 608 C; 606 G; 470 T;	Qy	
Oue Best Matc	<pre>uery Match 100.0%; Score 2094; DB 24; Length 2094; lest Local Similarity 100.0%; Pred. No. 0.00e+00; latches 2094; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</pre>	g &	
	tgacgcc 	d y	1081 gacctccttagccctgtctgctaggcgctggggagactgataacttggggaggcaagaga 1140 
		a y	1141 ctgggagccacttctccccagaaagtgtttaacggttttagcttttataataccttgt 1200 
	GOTGAGCACCCGGGTLGGGCCAGGALCCCGGCAGGCLGALCCCGT	do Qy	1201 gagagcccattcccaccattctacctgaggccaggacgtctggggtgtggggttggtgg 1260 
	ggagt 	da ya	1261 gtctatgttccccaggattcagctattctggaagatcagcacctaagagatgggactag 1320 
		8 %	1321 gacctgagcctggtcctggccgtccctaagcatgtgtcccaggagcaggacctactagga 1380 
		d y	1381 gagggggccaaggtcctgctcaactctaccctgctcccattcctccctc
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                                                                                                              30-NOV-1993; US-160067.
07-OCT-1994; US-320157.
(LXRB-) LXR BIOTECHNOLOGY INC.
MPI; 95-215106/28.
P-PSBB: R77876.
New nucleic acid sequences encoding Cdn apoptosis modulators - and related vectors, transformed cells, proteins and antibodies, useful or diagnosis and treatment e.g. of HIV infection, reperfusion injury
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                                                         hepatitis, osteoporosis;
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Pred. No. 0.00e+00;
0; Mismatches 0;
                                                          injury;
                                                  Cdn-1; apoptosis modulator; adoptive autoimmune disease; reperfusion injur shock; lymphoma; eczema; ss.
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Local Similarity 100.0%;
                                      (first entry)
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Matches 2072; Conservative
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W09515084-A.
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30-NOV-1994; U13930.
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CTTCCTCTCTCTCTTATAGACACTTGCTCCCAACCCATTCACTACAGGTGAAGGCTCTCAC 1633
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                        tctggcacagtgtaatccaggggtgtagatgggggaactgtgaatacttgaactctgttc
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                                                                                                                        Human Cdn-2 DNA.
Cdn-2; apoptosis modulator; adoptive immunotherapy; therapy; HIV
autoimmune disease; reperfusion injury; hepatitis, osteoporosis;
shock; lymphoma; eczema; ss.
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Claim 6; Fig.5A-H; 66pp; English.
Claim 6. Fig.5A-H; 66pp; English.
Cdn-2 cDNA was isolated from a human placental genomic library using a 950 bp fragment of Cdn-1 cDNA. Expression of Cdn-2 in mouse progenitor B-cell FL5.12 cells decreased IL-3-induced apoptosis. The Cdn-2 protein displayed 97% amino acid identity with Cdn-1 (R77876).
Sequence 6511 BP; 1513 A; 1620 C; 1605 G; 1773 T;
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mo9515084-A.
08-JUN-1995.
30-NOV-1994; U13930.
30-NOV-1994; US-160067.
07-0CT-1994; US-320157.
(LXRB-) LXR BIOTECHNOLOGY INC.
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095493 standard; DNA; 6511 (095493)
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Best Local Similarity 97.3%;
Matches 2026; Conservative
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WPI; 95-215106/28.
P-PSDB; R77877.
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             Location/Qualifiers
65..700
                                                                                          New isolated human Bcl-Y protein
treating disorders characterised
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larity 99.5%;
Conservative
                                             09-AUG-1995; U10103.
09-AUG-1994; US-287427.
11-OCT-1994; US-321071.
(IMMU-) IMMUNOGEN INC.
                                                                                                                                                                                                Similarity
                                                                       Chittenden TD;
WPI; 96-139648/14.
 SS.
                                                                                     P-PSDB; R81451
                          /*tag= a
WO9605232-A1.
22-FEB-1996.
                                                                                                           death
 therapy;
       sapiens
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T17375;
02-JUL-1996 (first entry)
Bcl-Y cDNA.
Bcl-Y; apoptosis; cell proliferation; cell death; diagnosis;
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A full-length cDNA clone (T17375) codes for Bcl-Y (R81451), a profein that induces apoptosis in cells and functions as a negative regulator of Bcl-2 function. It was isolated from a Jurkat cell cDNA library using as probe a partial Bcl-Y cDNA clone obtd. by PCR of DNA derived from the Namalwa cell line. The cDNA can be use for prodn. of recombinant Bcl-Y, as a probe, to produce transgenic animal models, and in the gene therepy of disorders characterised b inappropriate cell proliferation or cell death.

Sequence 1968 BP; 382 A; 560 C; 576 G; 450 T; cotgoagoccacggoagaatgoctatgagtacttcaccaagattgccaccagcctgtt tgagagtggcatcaattggggccgtgtggtggctcttctgggcttcggctaccgtctggc gatggtcaccttacctctgcaacctagcagcaccatggggcaggtgggacggcagctcgc catcatcggggacgacatcaaccgacgctatgactcagagttccagaccatgttgcagca CCTGCAGCCCACGCAGAGAATGCCTATGAGTACTTCACCAAAGATTGCCACCAGCGTGTT 9 Score 1886; DB 19; Length 1968; Pred. No. 0.00e+00; 0; Mismatches 0; Indels 9; develop by inappropriate

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1716 gccctgccctctgcttctgaggagcaggtagcccaggacatggagg-ggttttccgcagc 1774
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1665..1931
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W09515084-A.

08-JUN-1995.

30-NOV-1994; U13930.

30-NOV-1994; US-160067.

07-OCT-1994; US-320157.

(LXRB-) LXR BIOTECHNOLOGY INC.

Barr PJ, Klefer MC;

WPI; 95-215106/28.
                                                                                                                                                                                                                                                                               BP.
                                                                                                                                                                                                                                                                                                                    Human Cdn-3 DNA.
Cdn-3; apoptosis modulator;
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Best Local Similarity 89.6%;
Matches 1880; Conservative
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Q95494 standard; DNA; 5408
Q95494;
21-NOV-1995 (first entry)
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Sequence 5408 BP; 1369 A; 1384 C; 1314 G; 1341 T; autoimmune disease; reperfusion injury; hepatitis, osteoporosis; shock; lymphoma; eczema; ss. Score 1496; DB 14; Length 5408; Pred. No. 0.00e+00; 0; Mismatches 186; Indels 33;

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Epstekin-Barr Virus; BHRF1; fusion protein; epitope tag;
drug screening; co-practiottation; ELISA; immunoassay; antibody;
protein interactive trapping; virucide; antitumour; diagnostic;
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Location/Qualifiers
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Domain 479..1047
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Modified -site 277..279
/label= N-glycos_site
Modified -site 349..351
/label= N-glycos_site
Modified -site 600..602
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22-JUN-1990; U03586.
23-JUN-1989; US-370673.
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signal sequence
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Modified -site 195..1
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Modified -site 35..37
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Modified -site 161..1
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                                                                                      The sequence encodes Bax-2 protein, which is a bcl-1 homologue which interacts with Epstein-Barr virus (EBV) early lytic cycle BHRE1 protein, and is capable of modulating apoptosis. The Bax-2 gene is located on human chromosome-20. The protein may be used in complete or partial form, or as an epitope tag fusion protein, in a new virucide drug screening method, which involves combination of Bax-2 protein and a viral protein (e.g. EBV BHRE1), exposure to a test compound, and monitoring for disruption of the interaction of Bax-2 and viral protein interactive trapping or ELISA. Interaction of Bax-2 and viral proteins allows viral replication or latency in the absence of apoptosis. Compounds which inhibit the interaction may be used as virucide, antitumour or diagnostic agents. Sequence 1286 BP; 298 A; 341 C; 328 G; 319 T;
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                                         Screening for anti-viral agents - by detecting the ability of
                                                       agent to disrupt the interaction of a Bak protein and a viral
                                                                                                                                                                                                                                                  / Match 42.2%; Score 883; DB 24; Length 1286; Local Similarity 98.1%; Pred. No. 0.00e+00; os 916; Conservative 0; Mismatches 15; Indels 3
                                                                             Disclosure; Fig 2; 24pp; English.
(LXRB-) LXR BIOTECHNOLOGY INC
           Barr PJ, Kiefer MC;
WPI; 96-485886/48.
                               P-PSDB; W03669
                                                                                                                                                                                                                                                    Query Match
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1075 gtggcagccctgaacttgggcaatggtcccatcctgaacgtgctggtggttctgggtgtg 1134
                                                                                                                                                 gttctgttgggccagtttgtggtacgaagattcttcaaatcatgactcccaagggtgcct 1194
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The sequence was derived from the DNA encoding natriuretic peptide receptor B, NPRB, having quanyl cyclase (GC) activity and protein kinase activity. The DNA can be inserted into expression vectors for the prode. of the protein, opt. after being mutated to produce NPRB analogues. The protein has a mol wt. of 115 kD (calculated Mr-114,952). The protein (or variants) can be used in treatment of natriuretic peptide disorders, and also to isolate peptides using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NPRB; ANP; BNP; CNP; kidney failure; heart failure; protein kinase; hyperaldosteronism; glaucoma; guanyl cyclase. Homo sapiens.
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//abel- extracellular domain
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Domain 456..456
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ed -site 24..26
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Human Natriuretic Peptide Receptor B.
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US-08-320-157-6.rng

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                                                                                                                                                                                                                                                  hyrtnvrtgnsankngnnvvtnhghnnwtaraannyndartddrnhyntnngvnnanngs 194
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    can
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Antibodies with affinity for NPRB
                                                            Length 1047;
                                                                                          Conservative 293; Mismatches 618; Indels
                                51 T;
                                                                              4.06e-46;
                               83 G;
                                                              DB 2;
                                                           4.5%; Score 95;
                               15 C;
                                                                             Pred. No.
                             87 A;
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affinity chromatography.
also be prepd.
                             1047 BP;
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les 93; Conser
                  prepd
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Matches
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Gaps 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       194 snnsvnhnvyarnnggnnnathnnrangrnvyncgnnnmnhnnnnnnanrnnntngdyvnn 253
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The sequence was derived from the DNA encoding natriuretic peptide receptor B, NPRB, having quanty cyclase (GC) activity and protein kinase activity. The DNA can be inserted into expression vectors for the prodn. of the protein, opt. after being mutated to produce NPRB analogues. The protein has a mol Wt. of 115 kD (calculated Mr—114,952). The protein (or variants) can be used in treatment of natriuretic peptide disorders, and also to isolate peptides using affinity chromatography. Antibodies with affinity for NPRB can
                                                                                              09-APR-1991 (first entry)
Human Natriuretic Peptide Receptor B.
NPRB; ANP; BNP; CNP; kidney failure; heart failure; protein kinase;
hyperaldosteronism; glaucoma; guanyl cyclase.
               218
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274 TCCTCAGAAGCAGGGCAGGCCAGGCTCCCCCACCTGGGAGGACCTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 8.8%; Pred. No. 2.35e-34;
Matches 72; Conservative 234; Mismatches 503; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Natriuretic protein receptor B - for diagnosis and treatment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 T;
                                                                                                                                                                                                                                                                               'note= "binds natriuretic peptides A,B and C]"
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                                                                                                                                                                                                                                                                                                                                                    re= "GC and protien kinase activity"
lfled -site 24..26
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                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                  Johnson Label transmembrane domain 479..1047
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                                                                                                                                                                                                                                                  23..455
extracellular domain
                                         LT 8
Q10572 standard; DNA; 1047
Q10572;
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Chang M, Goeddel D, Lowe D;
WPI; 91-036711/05.
N-PSDB; Q10324.
                                                                                                                                                                                                                                                                                                                                        'label = cytoplasmic domain
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/label= N-glycos_site
Modified -site 195..197
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Modified -site 244..246
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Modified -site 277..279
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dodified -site 349..351
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/label= N-glycos_site
Modified -site 35..37
/label= N-glycos_site
                                                                                                                                                                                                     /label= signal sequence
Protein 12
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23-JUN-1989; US-370673.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= N-glycos_site
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                                                                                                                                                                                                                                   /label= mature NPBR
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                                                                                                                                                           Homo sapiens.
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269 IGAGGAGCAGGIAGCCCAGGACACAGAGGAGGTTTTCCGCAGCTACGTTTTTACCGCCA 328
                                                                                                                                                      yhgvtgnvvmdknndrntdnvnwamgdndsgdnnnaahysganknnwwtgrnnnwvkgan 432
                                                                                                                                                                                                       388 TACCTCGCAACCTAGCAGCACCATGGGGCCAGGTGGGACGCCAGCTCGCCATCATCGGGG 447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         805 AGTITGIGGIACGAAGAIICIICAAAICAIGACICCCAAGGGIGCCCTIIGGGICCCGGI 864
                                                     nnnrarndngvnngnsnmnnnagcnydgnnnyanvnnntnnnggtrndgnrnvnkmngrr
                                                                                      553 vakkranatravannakhmrdvanahatrangacadanaacavtaycargsandanand-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATCAAITGGGGCCGIGIGGGGGCTCITCIGGCIICGGCIACCGICIGGCCCTACACGI
                                                                                                                                                                                                                                                                                                                                                                                                                 ACG-GCAGAGAATGCCTATGAGTACTTCACCAAGATTGCCACCAGCCTGTTTGAGAGTGG
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Oligonucleotide probe MK14-A consists of nucleotides 5-95 of MK14
(Q51735). It hybridized to all app. of mycobacteria tested, but
cross reacted to a few non-mycobacterial app. The probe may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New oligo:nucleotide probes specific for Mycobacteria - used for detection and amplification of Mycobacteria nucleic acid in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAY-1994 (first entry)
Oligonucleotide probe MK14-A
Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       970 vgnkmnrycnngdtvnt-asrmnsngnanknhvssttkd 1007
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EP-571911-A.
D-DEC-1993.
24-MAY-1993; 108325.
26-MAY-1992; US-889651.
(BECT) BECTON DICKINSON CO.
Shank DD, Spears PA;
WPI; 93-378844/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q51746 standard; cDNA; 91 BP.
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1 Lehtovaara P. Knowles J. Kolvula A. Bamford J. Reinikainen T.

1 Lehtovaara P. Knowles J. Kolvula A. Bamford J. Reinikainen T.

2 Lehtovaara P. Knowles J. Kolvula A. Bamford J. Reinikainen T.

2 Lehtovaara P. Knowles J. Kolvula A. Bamford J. Reinikainen T.

2 Introducing random point mutations into nucleic acods -

2 Introducing random point mutations were introduced into the alpha fragment of

3 Ingle suranded template and an oligonucleotide was hybridised to

3 Ingle stranded template and an oligonucleotide was hybridised to

3 Ingle stranded template and an oligonucleotide was hybridised to

3 It to generate a popn of DRA molecules which terminate at all

4 possible nucleotide positions within a specified region. The

5 Variable J. ends generated in this way are used as primers for

5 It to generate and the molecules are ompleted to forms that can be

5 It ranscriptase and the molecules are completed to forms that can be

5 It sequence covers all 176 difft base substitutions, most of which

5 Sec also PROSTIN
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                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                     3 ctccggcgssvhsyyvvhvvshhhsvhhvvhhvhvsvvvvhhvvhvhhvhyhvyvsvc 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1580 CTCTCCTTATAGACACTTGCTCCCAAACCCATTCACTACAGGTGAAGGCTCTCACCC 1635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    137 vybbbvynvhnhnncncccbnnhvchnvhbnnhrnwayvrhdarrddvhccvchcc 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N81164;
08-NOV-1990 (first entry)
08-NOV-1990 (first entry)
Ease substituted E.coll beta-galactosidase alpha-fragment.
E.coll beta galactosidase alpha-fragment; base substitutions; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108 Others;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Base substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions;
Escherichia coli.
be useful as an initial screen for mycobacterial infection.
See also Q51735-45 and Q51747-59.
Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
                                                                                 Score 43; DB 9; Length yi, Pred: No. 1.89e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.1%; Score 44; DB 1; Length 204; 1.2%; Pred. No. 4.60e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .T 11
N81164 standard; DNA; 204 BP.
                                                                                                                                                                                                                                                                                                                                                       JT 10
N81164 standard; DNA; 204 BP
                                                                                                        y Match
Local Similarity 10.2%;
hes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 A;
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Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   08-NOV-1990 (first entry)
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30-MAR-1988; 105163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
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                                                                                                          Query Match
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                                                                                                                                                             Matches
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Introducing random point mutations into nucleic acods -
Introducing random point mutations into nucleic acods -
Introducing random point mutations into nucleic and screening.

This corporation, completion of molecules and screening.

Disclosure; p; English.

Random point mutations were introduced into the alpha fragment of consistences and solutained as a single stranded template and an oligonucleotide was hybridised to it to generate a popn of DNA molecules which terminate at all consistence included the possible nucleotide positions within a specified region. The reverse transcriptase and the molecules are misincorporated by the ranscriptase and the molecules are completed to forms that can be amplified and then expressed in a suitable host-vector system.

The sequence covers all 176 difft base substitutions, most of which consists possible in any given mutant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                      47 C; 17 G; 11 T; 108 Others;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nsed for
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                                                                                                                        (SUSO) SUOMEN SOKERI OY.
Lehtovaara P, Knowles J, Kolvula A, Bamford J, Reinikainen T;
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Oligonucleotide probe MK14-A consists of nucleotides 5-95 of (Q51735). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59.
Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-MAY-1994 (first entry)
Oligonucleotide probe MK14-A
Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 93-378844448.
New oligo:nucleotide probes specific for Mycobacteria - used detection and amplification of Mycobacteria nucleic acid in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 42; DB 9; Length 91; Pred. No. 7.69e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 45; DB 1; Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 1.11e-12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56; Mismatches
           /function=multiple cloning site primer_bind 187..204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
EP-571911-A.
01-DEC-1993.
24-MAY-1993; 108325.
26-MAY-1993; US-889651.
(BECT ) BECTON DICKINSON CO.
Shank DD, Spears PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O51746 standard; cDNA; 91 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.18;
Local Similarity 10.48;
les 10; Conservative
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Similarity 5.8%;
3; Conservative
                                                                         05-MAY-1988;
30-MAR-1988; 105163.
03-APR-1987; US-034819.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                      204 BP;
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                                                /*tag= b
EP-285123-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              samples
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65-APR-1995 (first entry)
Generic DNA sequence to generate a random TSAR petide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concateneated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         515 CTCTGCCGTGGGCTGCAGGTGCTGCAACATGGTCTGGAACTCTGAGTCATAGCGTCGGTT 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 bnnbnnbnnbnnbtgcnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnn 65
1778 GGTGTTGATAGTCCTTCTCCCCACTTAGAACCCTCCCAGATGAACTCCCTACTC 1727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 114;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     455 GATGTCGTCCCCGATGATGCCGAGCTGCCGTCCCACCTGCCCATGGTG 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.8%; Score 37; DB 12; I
5.5%; Pred. No. 7.46e-08;
vative 32; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                 /*tag= a
/note= "this sequence represents 'Z'; Z can be
sequence of 6, 9 or 12 nucleotides (see
                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                  CT 13
Q70465 standard; DNA; 114 BP.
Q70465;
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(UYNC-) UNIV NORTH CAROLINA.
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Q70468 standard; DNA; 114
Q70468;
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                                                                                                                                                                                                                                                                                                                                        misc_feature
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01-FEB-1993;
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                                                                                                                                                                                                                                                                                     Synthetic.
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ID 07
AC 07
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63

12 svhsyyvvhvvshhhsvhhvvhvvhvvhhvvhvvhhvhyhvyvsvctc

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5 gcnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbtgctgcnnbnnbnnbnnbnnbn 64
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     ద
                                                                                                                                                                                                                                                                      FT sequence or b, y or if nucleotides (see comments)*

W0941318-A

W09413-A

W09
                        Generic DNA sequence to generate a random TSAR petide library. TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                                                                                                   'Z'; Z can be a
                                                                                                                                                                                                                                   s sequence represents 'Z'; Z
6, 9 or 12 nucleotides (see
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                                                                                                129 GGAGATGGAGGTCCGAGGGCTGCTGCTCCTCCCAGGGGCTGAGTGGGAGCCCAGT 70
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     Length 114;
 Score 36; DB 12; Length 114 Pred. No. 2.86e-07; 31; Mismatches 69; Indels
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9
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OLT 15
Q70466 standard; DNA; 114 BP.
Q70466;
Q70466;
Q50467;
Q50467;
Q50471995 (first entry)
Genoric DNA sequence to generate a random TSAR-9 petide library.
TSAR; totally synthatic affinity reagent; synthetic; binding domain;
effector domain; concateneated heterofunctional protein; linker;
effector tapid; detection; screening; treatment; generic; ss.
Synthatic.
Location\*\*Concation\*\* 

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Treating proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins or promprising a binding domain and an effector domain bisclosure; Page 35; 255pp; English and English and an effector domain bisclosure; Page 35; 255pp; English and Engli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 114;
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                                                                                             sequence represents 'Z'; Z
5, 9 or 12 nucleotides (see
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US-176500.
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01-FEB-1994;
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65 nbnnbnnbnnbnnbnnbnnbtgcnnbnnbnnbnnbnnbnnbnnbnnb 114 625 TCTACCAGCATGCCCTGACTGCCTTCCTAGGCCAGGTGACCCGCTTCGTG 674 Search completed: Thu Aug 21 10:38:25 1997 Job time : 628 secs. 셤 à

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Gaps

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7.3%; Pred. No. 4.05e-06;

30; Mismatches

8; Conservative

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129:EST129
134:EST134
139:EST139
144:EST144
149:EST149
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    n.a. database search, using Smith-Waterman algorithm

                                                                                                                                                                                                                                                                                                                                                                        Release 2.1D John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by IntelliGenetics, Inc.
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128:EST128
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138:EST138
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173:EST173
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5 106:EST106 107:EST107 10
111:EST111 112:EST112 11
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0 121:EST121 122:EST122 12
126:EST126 127:EST127 12
126:EST131 132:EST132 13
131:EST131 132:EST132 13
136:EST136 137:EST132 13
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EST172
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CTCCTAGATGTCCCCTGTTC.
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Perfect Score:
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Description

yu36g10.rl Homo sapie 0.00e+00

yu36g10.rl Homo sapie 0.00e+00

mg88g02.rl Soares mou 0.00e+00

mb16g04.rl Soares mou 0.00e+00

mj39b01.rl Soares mou 0.00e+00

mj39b01.rl Soares mou 0.00e+00

mj39b01.rl Soares mou 0.00e+00

mj09a0.rl Soares mou 0.00e+00

mj08a0.rl Soares mou 0.00e+00

mj08a0.rl Soares mou 0.00e+00

my08a0.rl Soares mou 0.00e+00

my16b12.rl Soares mou 0.00e+00

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yz73c08.rl Homo sapie 0.17e-06

yz73c08.rl Homo sapie 6.17e-06

yc49b08.rl Homo sapie 6.17e-06

yc49b08.rl Homo sapie 6.17e-06

yc49b08.rl Homo sapie 6.17e-06

yc49b08.rl Homo sapie 1.59e-03

H. Sapiens partial cD 1.04e-04

yc7cd12.sl Soares ret 1.59e-03

r x5d101.rl Homo sapie 1.59e-03

yc45d07.rl Soares fet 1.59e-03

zad1a1.rl Homo sapie 1.59e-03

zb14a04.rl Homo sapie 1.59e-03

zb14a04.rl Soares fet 1.59e-03

zb14a04.rl Soares fet 1.59e-03

zb22c08.rl Homo sapie 1.59e-03

zb12c08.rl Homo sapie 1.59e-03

zb2a09.sl Soares fet 1.59e-03

zb2a09.sl Soares fet 1.59e-04

yg5509.rl Homo sapie 1.04e-04

yg5509.rl Homo sapie 1.04e-04
                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
 179:EST179
184:EST184
189:EST189
194:EST194
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177:EST177 178:EST178 178:EST181 182:EST182 183:EST183 1818:EST183 1818:EST188 115 192:EST192 193:EST193 115:EST197 EST197 EST197 EST197
                                                                                                           scale 5.307
                                                                                                           Variance 2.224;
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W23886
AAA49828
AAA69828
W82028
W82028
W7319
AA139013
H31839
H31839
T58949
T76889
H15311
R39042
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R85722
HSB73E022
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W80365
W57984
HUM519C08B
175:EST175 176:EST176 1
180:EST180 181:EST181 1
185:EST185 186 EST186 1
190:EST190 191:EST191 1
195:EST195 196:EST196 1
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H52673
AA016399
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AA169681
R22823
T54824
W17230
W02475
AA01628
AA036957
AA0166773
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18-SEP-1995

clone=235938 primer=M13RP1 library-Soares ovary tumor NbHOT

yu36g10.rl Homo sapiens cDNA clone 235938 5' H52672 9992513

RESULT 1 LOCUS DEFINITION ACCESSION NID KEYWORDS SOURCE

ALIGNMENTS

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RESULT 2
LOCUS
DEFINITION
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                 (ampicillin resistant) Raitel-Not I Rsite2-Eco RI Female. Ist Strand obbt was primed with a Not I - oligo(df) primer [5' strand obbt was primed with a Not I and off primer 3', double-stranded cDNA was size selected, ligated to Eco RI adapters double-stranded cDNA was size selected, ligated to Eco RI adapters obbtamacia), dispessed with Not I and cloned into the Not I and Eco RI sites of a modified pi713 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo.
                                                                                                                                                             Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Barcopterygil; Choanata; Tetrapoda; Anniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhin; Hominidae; Homo.
1 (bases 1 to 409)
1 (bases 1 to 409)
1 (bases 1, Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Hultman,M., Rucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Wallerskis,E., Materston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stops: 307
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rector-pT7T3D (Pharmacia) with a modified polylinker host-DH10B
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WashU-warck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watsoo.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 355; DB 84; Length 409;
Pred. No. 0.00e+00;
0; Mismatches 11; Indels 5;
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Bost Local Similarity 96.1%;
Matches 390; Conservative
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Bukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygil; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archorta; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 449)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Hultman, M., Rucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Tan, F., Tan, F., Materston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 339; DB 84; Length 449;
Pred. No. 0.00e+00;
0; Mismatches 13; Indels 11; Gaps 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washurderck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: est@watson wustl.edu
High quality sequence stops: 379
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                    clone=235938 primer=Promega -21m13 library=Soares ovary tumor
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yu36g10.s1 Homo saplens cDNA clone 235938 3' H52673
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/organism="Homo sapiens"
/clone="235938"
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Best Local Similarity 94.5%;
Matches 413; Conservative
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Query Match 12.8%;
Best Local Similarity 78.1%;
Matches 371; Conservative
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H56462
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                                                                                                                                                                                                                                                                                                                                                                  1 (bases I to 497)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Galsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                              Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                      4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Soares mouse embryo NbMEl3.5 14.5" /sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Possible reversed clone: similarity on wrong strand Seq primer: -28M13 rev2 from Amersham High quality sequence stop: 484.

Location/Qualifiers
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/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                      The WashU-HHMI Mouse EST Project
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Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Barcopterygii; Choanata; Tetrapoda; Anniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 303)
Hillier,L., Clark,N., Dubuque,T., Elliston,R., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohling,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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                                                                                                                                                                                                                                                                                                   382 tcgtaggcattcccggctgtgggctgaagctgttctagtaaattctggaactctgtgtcg 441
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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   Length 497;
                                       Indels
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Score 267; DB 155; 1
Pred. No. 0.00e+00;
0; Mismatches 104;
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Query Match 11.8%;
Best Local Similarity 77.9%;
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Gelel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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Soares mouse p3NMF19.5 Mus musculus cDNA clone 329622
SW:BCLX_HUMAN Q07817 APOPTOSIS REGULATOR BCL-X. ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:211022
            High quality sequence stops: 251
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@limage.llnl.gov) for further information.
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 gaggagcaggtagcccaggacacagaggaggttttccgcagctacgttttttaccaccat 120
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Pred. No. 0.00e+00;
0; Mismatches 14; Indels
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
Tol: 34 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
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                                                                                                            /organism="Homo sapiens"
/clone="231262"
<1..>303
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The WashU-HHMI Mouse EST Project
                                                                                   Location/Qualiflers
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Email: est@watson.wustl.edu
                                                                                                                                                                                                                 .ch 12.7%;
il Similarity 94.7%;
288; Conservative
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similar to 5
W42014
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ANNA EST 09-SEP-1996 mRNA EST 09-SEP-1996 mj33b01.rl Scares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone 478441 5' similar to SW:BCLX_HUMAN Q07817 APOPTOSIS REGULATOR AA049970 g1529641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        209 ctggcgatgtaatgatgcagtatgatatcagccaaaaagcaggtcacctggcccaggaag 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCGGtCaaaccacgctggtagacgtacagggccagacggtagccaaagcccaggagagcc 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 accacgcggccccagctgatgccactcttaaataggctggaggcgatcttggtgaagagt 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  389 tcgtaggcattcccggctgtgggctgaagctgttctagtagattctggaactctgtgtcg 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89 aagaatctgtgtaccacgaattggcccaacagaaccaccaaaaatcaccattacggtc 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   149 aggatggggactctacgaaaattcagggctgccacccaaccgcctctctgtgcgatccat 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5
                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 545;
Possible reversed clone: similarity on wrong strand Seq primer: Erprimer High quality sequence stop: 411.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                            /clone_lib="Soares mouse p3NMF19.5"
/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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Pred. No. 0.00e+00;
0; Mismatches 103;
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                                                                     1.545
/organism="Mus musculus"
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1 cctccctcagctctctgggacctccttagccctgtctgctaggcgctgggagactgata 60
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les 160; Conservative
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                 296
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Marrad., Hiller,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Marrad., Kucaba.,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
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                                                                                                                                                                                                                                                                                     Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                         Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176 cccaaccgcctctctgtgcgatccatctggcgatgtaatgatgcagtatgatatcagcca 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     236 aaaagcaggtcacctggcccaggaagccggtcaaaccacgctggtagacgtacagggcca 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56 agtgcgtccccggttgtcatgatctgaagaatctgtgtaccacgaattggcccaacagaa 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116 ccacaccaaaaatcaccattacggtcatgatggggtctctacgaaaattcagggctgcca 175
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                                                                                                                                                                                                                  Washington University School of MedicineP
4444 Forest Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Soares mouse embryo NbME13.5 14.5"
/sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 229; DB 138; Length 446;
Pred. No. 0.00e+00;
0; Mismatches 81; Indels 0
                                                                                                                                                                                                                                                                                                                                            Possible reversed clone: similarity on wrong strand Seq primer: -28M13 rev2 from Amersham High quality sequence stop: 319.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
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                                                                                                                                                                                                      Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
                                                                                                                                                               The WashU-HHMI Mouse EST Project Unpublished (1996)
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1 Similarity 79.3%;
310; Conservative
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                             Mus musculus
  EST.
house mouse.
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W23886 161 bp mRNA EST 20-AUG-1996
zb46a10.rl Soares fetal lung NbHL19W Homo sapiens cDNA clone 306618
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Wilson RK
WashJ-Merck EST Project
WashJ-Merck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: est@wastson.wustl.edu
This clone is available royalty-free through LLNL; contact the
INAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 988 Std Error: 0.00
Seq primer: mob.RGSA+ET.
Location/Qualifiers
356 ggctggaggcgatcttggtgaagagttcgtaggcatttccggctgtgggctgaagctgtt 415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases I to 161)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Helman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E.,
Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R..
Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
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Pred. No. 7.70e-255;
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/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="306618"
/clone_lib="Soares fetal lung NbHL19W"
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Query Match
Best Local Similarity 79.7%;
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Marra M/Mouse EST Project
Washington University School of MedicineP
Washington University School of MedicineP
4444 Forest Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
Fax: 315 286 1810
Fax: 315 286 1810
MGI:286320
MGI:286320
MGI:286320
1063 CCTCCCTCAGCTCTCTGGGACCTCCTTAGCCCTGTCTGCTAGGCGCTGGGGAGACTGATA 1122
                         Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                  AA049828 292 bp mRNA EST 09-SEP-1996 mj09a09.rl Scares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone 47576 5'.
AA049828 g1529499
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Pred. No. 3.82e-86;
0; Mismatches 29; Indels
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/dev_stage="13.5-14.5dpc total fetus"
/lab.host="DH108"
<1..>293
                                                                                                 121 tttttataatacccttgtgagaagcccattcccaccattct 161
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Location/Qualifiers
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3.4%;
Best Local Similarity 79.7%;
Matches 137; Conservative
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptce, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R. Mouse EST Project Unpublished (1996)
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Washington University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
4761-314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
Fax: 315 Far: 315 Far
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Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                    AAU50569 361 bp mRNA EST 09-SEP-1996 m16b12.rl Scares mouse embryo NbME13.5 14.5 Mus musculus CDNA clone 476255 5'.
127 ctccaccaagacctgaaaaatggcatctggacaaggaccaggtcccccgaaggtgggctg 186
                                            /clone_lib="Soares mouse embryo NbME13.5 14.5"
                                                                                                                                                                                                                                                                                                                                                 241 ctttcgaagctacgttttttacctccaccagcaggaacaggagcccagggg 292
                                                                                                                                                                                                                                                                                                                                                                                              Length 361;
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/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
<1..>361
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Pred. No. 3.82e-86;
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                                                                                                                                                                                                                       N83998 232 bp mRNA EST 01-APR-1996
KK4271F Homo sapiens cDNA clone KK4271 5' similar to BAK FOR BCL-2
  4
                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Barcopterygil; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
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DEFINITION mf02e01.rl Soares mouse p3NMF19.5 Mus musculus cDNA clone 403896
5'.
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                          196 ctccaccaagacctgaaaaatggcatctggacaaggaccaggtcccccgaaggtgggctg 255
                                        242 CGGAGAGCCTGCCCTGCCTTCTGAGGAGCAGGTAGCCCAGGACACAGGAGGT 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Molecular Cardiology
University of Toronto
Banting Institute, 100 College St., Toronto, Ontario, M5G1L5
Tel: 4169788758
Fax: 4169785650
  Gaps
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                                                                                                                                  Score 62; DB 133; Length 232;
Pred. No. 4.39e-67;
0; Mismatches 1; Indels
 Indels
 29;
Mismatches
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/clone="KK4271"
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Location/Qualifiers
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Unpublished (1996)
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Similarity 98.4%;
63; Conservative
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Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mouseest@watson.wustl.edu
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:247664
                                                        Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: -28M13 rev2 from Amersham.
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Mus musculus
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ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

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Tat primer=M13 - 21 library=Rat PC-12 cells, untreated vector=pBluescript SK- Rsitel=EcoRI Rsite2=XhoI poly(A)+ RNA was purified from untreated PC12 cells cultured for 9 days. cDNA was constructed using an oligo-dT primer and directionally cloned using the Lambda ZAP II Vector Kit by Stratagene.
                                                                                           Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3/); double-stranded CDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified py 773 vector. RNA provided by Dr. Bertrand Jordan. Library went through three rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."
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Vertebrata; Mammalla; Eutheria; Rodentia; Sciurognathi; Myomorpha;
Muridae; Murinae; Rattus.
1 (bases 1 to 408)
Lee, M.H., Weinstock, K.G., Kirkness, E.F., Earle-Hughes, J.A.,
Fuldner, R.A., Marmaras, S., Glodek, A., Gocayne, J.D., Adams, M.D.,
Kerlavage, A.R., Fraser, C.M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mouseest@watson.wustl.edu
This clone is available royalty.free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:361866
Eukaryotae, mitochondrial eukaryotes, Metazoa, Chordata,
Vertebrata, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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                                                                                                                                                                                                                                                                                                            Washu-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 320;
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Pred. No. 2.04e-26;
0; Mismatches 9; Indels
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E8T106322 Rattus sp. cDNA 3' end.
H31839
9977256
                                                                                                                                                                                                                   The Washu-HHMI Mouse EST Project
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/dev_stage="4 weeks"
/lab_host="DH10B"
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Best Local Similarity 84.2%;
Matches 48; Conservative
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1 (bases 1 to 445)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Gersel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schollenberg, K., Steptce, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Washu-HHMI Mouse EST Project
                 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mouseestewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.linl.gov) for further information.
MGI:244094
Seq primer: ETPrimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mr04a06.rl Soares mouse 3NbMS Mus musculus cDNA clone 596434 5's similar to TR:G595926 G595926 BAK-2 PROTEIN. ; G1701240
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                                                                                                                                                                                                                                                                                                       Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: mouseest@kwtson.wustl.edu
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2.1%; Score 44; DB 126; Length 445;
Best Local Similarity 72.1%; Pred. No. 9.87e-35;
Matchos 80; Conservative 0; Mismatches 30; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Soares mouse embryo NbME13.5 14.5"
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/lab_host-"DH10B"
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Location/Qualifiers
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Mus musculus
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RESULT 13

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NID KEYWORDS ACCESSION

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Tat primer-M13 Reverse library=Rat PC-12 cells, untreated vector=pBluescript SK- Rsitel=EcoRI Rsite2=XhoI poly(A)+ RNA was purified from untreated PC12 cells cultured for 9 days. cDNA was constructed using an oligo-dr primer and directionally cloned using the Lambda ZAP II Vector Kit by Stratagene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Myomorpha; Murinae; Rattus.

1 (bases 1 to 279)
Lee, M.H., Weinstock, K.G., Kirkness, E.F., Earle-Hughes, J.A., Fuldner, R.A., Marmaras, S., Glodek, A., Gocayne, J.D., Adams, M.D., Kerlavage, A.R., Fraser, C.M. and Venter, J.C.
Comparative expressed sequence tag analysis of differential gene expression profiles in PC-12 cells before and after nerve growth factor treatment
                                                                                                                                                                                                                                                                                                                                                                                                                         ÷
Comparative expressed sequence tag analysis of differential gene expression profiles in PC-12 cells before and after nerve growth factor treatment
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For clone availability please contact the TIGR Database
(tdbinfo@tdb.tigr.org)
                                                                                                                                                                                                              the TIGR Database
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 279;
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                                                 Proc. Matl. Acad. Sci. USA 92, 8303-8307 (1995)
Other ESTS: EST106323
Contact: Lee NH
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 301869943
Email: nhlee@tigr.org
For clone availability please contact the TIGR Da (tdbin6@tdb.tigr.org).
Location/Qualifiers
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Other_ESTS: EST106322
Contact: Lee NH
The Institute for Genomic Research
932 Clopper Rd, Galthersburg, MD 20878
Tel: 3018699056
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SEX106323 Rattus sp. cDNA 5' end.
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Best Local Similarity 71.4%;
Matches 80; Conservative
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Fax: 3018699423
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Description

Match Length DB

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AA1886334
AA185611
AA222196
MM1141069
AA242472
AA123834
AM123834
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1258 161 133 133 133 309 309 498 498 498 310 310 320

98 58 56 108

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Statistics:	Variance 2

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mt62e08.ri Soares 2Nb mt62e08.ri Soares 2Nb zk89a06.ri Soares pre zk89a06.si Soares pre yv67g01.si Soares fet human STS CHLC.UTR\_03 yv43f09.si Soares fet human STS WI-9107.

AA185558 AA185558 AA115608 AA115474 N58258 G15924 N53559

221 73 73 1104 13 14 44 25 38

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ALIGNMENTS

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AA020955 HS1174584 AA259189

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human STS WI-7983.

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my25611.rl Soares 2Nb 1.0
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my25611.rl Soares 2Nb 1.0
my25f11.rl Barstead m 6.mx21a06.rl Soares pre 2.14c11.sl Soares pre 2.14c11.sl Soares pre 2.14c11.sl Soares pre 2.14c11.sl Soares fet 9.vy51e02.sl Soares fet 9.vy51e02.sl Soares fet 9.vy51e02.sl Soares fet 9.xy54d04.sl Stratagene mod3f04.rl Stratagene mod my24f04.rl Stratagene mod my24f04.rl

DM36D7S T02955

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collection.

Homo sapiens

Bukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;

Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;

Tetrapoda; Anniota; Mammalia; Theria; Eutheria; Archonta; Primates;

Catarrhin; Hominidae; Homo.

(bases I to 1258)
                                                                                                                                                                                                                                                                                    Research; Physically
                       19-0CT-1995
                                                     G06794
g860039
STS sequence; primer; sequence tagged site.
human STSs derived from sequences in dbEST and the Unigene
                                                                                                                                                                                                                                                                                                                                                       Contact: Thomas Hudson
Whitehead Institute/MIT Center for Genome Research
Whitehead Institute for Blomedical Research
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Unpublished (1995)
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

& Query

Result

1376

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1557 TCCTCTCAGTTCTCTCCCTTCCTCTCTTATAGACACTTGCTCCCAACCCATTCACTA 1616
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/organism="Homo sapiens"

281.130

/map="751.A7; 787.E.4; 908.C.6; 923.D.2; 919.D.10;
942.A.12; 808.G.(6,11)"

281.130

/map="751.A7; 787.E.4; 908.C.6; 923.D.2; 919.D.10;
942.A.12; 808.G.(6,11)"

complement(606..625)

/map="751.A.7; 787.E.4; 908.C.6; 923.D.2; 919.D.10;
942.A.12; 808.G.(6,11)"

84.2.A.12; 808.G.(6,11)"

356 c. 355 g. 301 t. 10 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                957 CACTCCAGCTTCGGAGGCCCTGCGTGGGGGCCAGTCAGGCTGCAGAGGCACCTCAACATT 1016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gagactggggagccacttctccccagaaagtgtttaacggttttagctttttataataccc
                                                                                                                                                                                                                                                                                                                -- Unigene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1248; DB 38; Length 1258;
Pred. No. 0.00e+00;
0; Mismatches 10; Indels 0;
                                                                                                                                                                                                                                                                                                               with primer pairs derived from U16811 Location/Qualiflers
 Cambridge MA 02142 USA
                                                                                                                                                                           Template: 10 ng
Primer: each 5 pw
Prys: each 4 nm
Taq Polymerase: 0.025 units/ul
                                                     Primer A: CTGATAACTTGGGGAGGCAA Primer B: GAGAGTCCAACTGCAAAGGC STS size: 345
                                                                                                                        Ö
                                                                                                                     Annealing: 56 degrees C
Polymerization:
PCR Cycles: 35
Thermal Cycler:
                                thudson@genome.wi.mit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59.6%; (larity 99.2%; Conservative
                                                                                                                                                                                                                                                         MgCl2: 1.5 mM
KCl: 50 mM
Tris-HCL: 10 mM
pH: 9.3
                                                                                                                                                                                                                        Total Vol: 20 ul
9 Cambridge Center,
Tel: 617 252 1900
Fax: 617 252 1902
                                                                                                             Denaturation:
                                                                                                  Presoak:
                                                                                                                                                                                                                                                                                                                with
                                                                           STS size: 34 PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                   Protocol:
                                                                                                                                                                                                                                                                                                                Prepared
                                                                                                                                                                                                                                                                                                                                                                                                                                                            236
                                Ema 11:
                                                                                                                                                                                                                                                Buffer:
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Best Local Simil
Matches 1248;
                                                                                                                                                                                                                                                                                                                                                                                           primer_bind
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ORIGIN
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CDNA clone 306618
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; H
[1]
                                                                                                                                                                                            09-WAY-1996 (Rel. 47, Created)
07-WAR-1997 (Rel. 51, Last updated, Version 2)
2b46a10.rl Soares fetal lung NbHL19W Homo sapiens
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Unpublished.
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                                                                                                                                                                                    source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
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LOCUS
    ET FET FET SO
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                                                                                                                                                                                                                 double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of
                                                                                                                                                                                                                                                                                                                                      normalization to a cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NobHIJ9W."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1063 CCTCCCTCAGCTCTCTGGGACCTCTAGCCCTGTCTGCTAGGCGCTGGGGAGACTGATA 1122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 acttggggaggcaagagactgggagccacttctccccagaaagtgtttaacggttttagc 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 cctccctcagctctctgggacctccttagccctgtctgctaggcgctgggagactgata 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                    Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis, Mo 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through LLNL, contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 988 Std Error: 0.00 Seq primer: mob.REGA+ET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-FEB-1997 (Rel. 51, Created)
22-FEB-1997 (Rel. 51, Last updated, Version 2)
mt62a08.rl Soares 2NbMT Mus musculus cDNA clone 634454 5' similar
to TR:G595926 G595926 BAK-2 PROTEIN. ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Marra M., Hillier L., Allen M., Bowles M., Dietrich N., Dubuque T., Geisel S., Kucaba T., Lacy M., Le M., Martin J., Morris M., Schellenberg K., Steptoe M., Tan F., Underwood K., Moore B., Theising B., Wylle T., Lennon G., Soares B., Wilson R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ı,
         Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M.,
Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M.,
Parsons J., Rifkin L., Rohlfing T., Tan F., Trevaskis E.,
Waterston R., Williamson A., Wohldmann P., Wilson R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 154; DB 88; Length 16 Pred. No. 1.68e-256; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                        /clone="306618"
/clone_lib="Soares fetal lung NbHL19W"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA <1. >161
Sequence 161 BP; 33 A; 46 C; 38 G; 44 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T
MM1142620 standard; RNA; EST; 133 BP.
AA185611;
                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 99.4%;
Matches 160; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (house mouse)
                                                                         Unpublished
                                                                                                                                                                                                         source
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by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructedby Bento Soares and M.Fatima Bonaldo."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST 19-FEB-1997
CDNA clone 634454 5' similar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 ccgtccccttctggacagcaggttgcccatgacacagaggaggtctttcgaagctacgta 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, Mo 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.lln.gov) for further information. MGI:386446 Trace considered overall poor quality Possible reversed clone: similarity sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ő
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            y Match 2.6%; Score 55; DB 91; Length 133
Local Similarity 81.6%; Pred. No. 9.33e-55;
hes 71; Conservative 0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33 A; 40 C; 34 G; 26 T; 0 other;
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mt62a08.rl Soares 2NbMT Mus musculus
to TR:G595926 G595926 BAK-2 PROTEIN.
AA185611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Soares 2NbMT"
                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="Thymus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="4 weeks"
/lab_host="DH10B"
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"The WashU-HHMI Mouse EST Project";
                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                              /strain="C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="634454"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 133)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               house mouse.
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 2.6%;
Best Local Similarity 81.6%;
Matches 71; Conservative
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                                                                                                               MGI:386446
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DEFINITION
ACCESSION
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BASE COUNT
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SOURCE
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                                                                                                                                                                                                      FEATURES
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                                                                                                                                                                                                                                                       1 (bases 1 to 133)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schallenberg, K., Steptce, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA185611 133 bp mRNA EST 07-JAN-1997 mt62a08.rl Soaras 2NbWT Mus musculus CDNA clone 634454 5' similar to TR:G559206 G595926 BAK-2 PROTEIN, ;.
AA185611 g1769266
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Washington University School of MedicineP 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1810 Fax: 314 286 1810 Email: mousecst@watson.wustl.edu
Email: mousecst@watson.wustl.edu
Inis.clone is available royalty.free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:386446
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                           Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 55; DB 61; Length 133;
Pred. No. 9.33e-55;
0; Mismatches 16; Indels
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Washington University School of Medicinep
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Soares 2NbMT"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 ttttaccttcaccagcaggaacatgag 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   318 TTTTACCGCCATCAGCAACAGGAG 344
                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.6%;
Local Similarity 81.6%;
des 71; Conservative
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BASE COUNT
ORIGIN
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COMMENT
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SOURCE
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1 (bases 1 to 309)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA222196 309 bp mRNA EST 18-FEB-1997
mw21906.rl Soares mouse 3NME12 5 Mus musculus cDNA clone 671386 5/
g1842522
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Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 ccgtcccttctggacagcaggttgcccatgacacagaggggggtctttcgaagctacgta 100
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WashU-HMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                         Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28Mi3 rev2 from Amersham
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 133;
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Pred. No. 9.33e-55;
0; Mismatches 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="634454"
/clone_lib="Soares 2NbMT"
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/lab_host="DH10B"
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/organism="Mus musculus"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
                                                                                                                                                                                 total mouse RNA [providedby Minoru Ko, Wayne State Univ.]; double-Stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. Library wen
                                                                                                                                                                                                                                                                                                            through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."
/clone="671386"
/clone_lib="Soares mouse 3NME12 5"
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Schellenberg,K., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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mx26g11.r1 Soares mouse NML Mus musculus cDNA clone 681380 5.
AA.242472
91873149
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91; Length 309;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <1..>309
59 A; 92 C; 91 G; 67 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                               /sex="unknown"
/dev_stage="12.5dpc total fetus"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 44; DB 91;
Pred. No. 3.05e-35;
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             'organism="Mus musculus"
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Best Local Similarity 72.1%;
Matches 80; Conservative
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This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI.411090
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 122.
Location/qualiflers
1.309
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0-FEB-1997 (Rel. 51, Created)
20-FEB-1997 (Rel. 51, Last updated, Version 1)
mw21906.rl Soares mouse 3NME12 5 Mus musculus cDNA clone 671386 5'
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Dubuque T., Geisel S., Kucaba T., Lacy M., Le M., Martin J.,
Morris M., Schellenberg K., Steptoe M., Tan F., Underwood K.,
Moore B., Theising B., Wylie T., Lennon G., Soares B., Wilson R.,
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Pred. No. 3.05e-35;
0; Mismatches 30; Indels
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                                                                                                                                                                               /organism-"Mus musculus"
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AA222196;
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"The WashU-HHMI Mouse EST Project";
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Best Local Similarity 72.1%;
Matches 80; Conservative
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AUTHORS
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                                                                                                                                                                                                                                                                             198 tetectaccecaatecatecttttgeettggggetggaeteteagggattetgageee 257
                                                                                                                                                                                                       Gaps
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Dubuque T., Geisel S., Kucaba T., Lacy M., Le M., Martin J.,
Morris M., Schellenberg K., Steptoe M., Tan F., Underwood K.,
Moore B., Theising B., Wylie T., Lennon G., Soares B., Wilson R.,
Waterston R.,
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               11-MAR-1997 (Rel. 51, Created)
11-MAR-1997 (Rel. 51, Last updated, Version 1)
mx26911.rl Soares mouse NML Mus musculus cDNA clone 681380
                                                                                                                                                                             Score 42; DB 67; Length 498;
Pred. No. 7.47e-32;
                                                                                                                                                                                                     0; Mismatches 43; Indels
                                                                       /clone="681380"
/clone_lib="Soares mouse NML"
/tissue_type="Liver"
/lab_host="DH108"
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                                                                                                                                        109
                                                                                                                                                                                                                                                                                                                                                                                                            MM1158998 standard; RNA; EST; 498 BP
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llarity 67.4%;
Conservative
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Best Local Similarity (
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BASE COUNT
ORIGIN
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1 (bases 1 to 310)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Galsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mp93c04.rl Soares 2NbMT Mus musculus cDNA clone 576774 5' sAmilar to TR:0595926 G595926 BAK-2 PROTEIN. ;
                                                                                                                                                                                                                                              Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                      198 totoctaccocaatccatccattttgccttggggctggactctcagggattctgagccc 257
                                                                                                                                    Score 42; DB 92; Length 498;
Pred. No. 7.47e-32;
                                                                                                                                                                                   Indels
                                                                                                   99 A; 166 C; 124 G; 109 T; 0 other;
                                                                                                                                                                                   0; Mismatches 43;
                       mouse NML"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: -28M13 rev2 from Amersham
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Soares 2NbMT"
/sex="male"
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The WashU-HHMI Mouse EST Project
Unpublished (1996)
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                                     /tissue_type="Liver"
/lab_host="DH10B"
<1..>498
                  /clone_lib-"Soares
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain-"C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="576774"
/clone-"681380"
                                                                                                                                        2.0%;
Local Similarity 67.4%;
                                                                                                                                                                                   91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            1537 TCCAAGCCTGCCTCC 1551
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Mus musculus
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JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                    ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                          KEYWORDS
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                                                                                                                                                   ctccaccaagacctgaaaatggcatctggacaaggaccaggtcccccgaagtgggc-tg 243
                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, Mo 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:351422 Seq Primer: -28M13 rev2 from Amersham.

Key
                                                                                                                                                                                                                                                                                                      25-NOV-1996 (Rel. 50, Created)
19-FEB-1997 (Rel. 51, Last updated, Version 2)
mp93c04.rl Soares 2NDMT Mus musculus cDNA clone 576774 5' similar
to TR:G595926 G595926 BAK-2 PROTEIN.;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Marra M., Hillier L., Allen M., Bowles M., Dietrich N., Dubuque T., Gelsel S., Kucaba T., Lacy M., Le M., Martin J., Morris M., Schellenberg K., Steptoe M., Tan F., Underwood K., Moore B., Theising B., Wylie T., Lennon G., Soares B., Wilson R., Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (house mouse)
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                               7;
                        others
                                                        Length 310;
                                                       Score 40; DB 7; Length 310;
Pred. No. 1.60e-28;
0; Mismatches 22; Indels
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                      55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Soares 2NbMT"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                        ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The WashU-HHMI Mouse EST Project";
                        б
                                                                                                                                                                                                                                                                      standard; RNA; EST; 310
/lab_host-"DH10B"
                      98
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                                                     1.9%;
ilarity 78.2%;
Conservative
                      96
C
            <1..>310
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                                                                   Similarity
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                      72
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                                                                             104;
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AA123834;
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Best Local (
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                         AA123834 310 bp mRNA EST 17-FEB-1997
1093c04.r1 Soares 2NbMT Mus musculus cDNA clone 576774 5' similar
10 1R:6555926 G595926 BAK-2 PROTEIN: ;.
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Washidyon University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty.free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                   244 cgatgagtc--ccc-gtcc-c--cttctgaacagcaggttgcccaggacacagaggt 297
                                                                                                                                                                                                                                       7; Gaps
                                                        Length 310;
                                                                                                 Indels
                                                      Score 40; DB 98; Le
Pred. No. 1.60e-28;
0; Mismatches 22;
mRNA <1..>310
Sequence 310 BP; 72 A; 96 C; 86 G; 55 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGI:351422
Seq primer: -28M13 rev2 from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Soares 2NbMT"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
<1..>310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                      Query Match 1.9%;
Best Local Similarity 78.2%;
Matches 104; Conservative
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Gaps

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BASE COUNT ORIGIN

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3']; double-stranded cDNA wasiigated to Eco RI adaptors [GTTGGATTCGGTACC], digested with Not I and cloned into t Not I and Eco RI sites of the modified pT/T3 vector. Library constructed by Bob Barstead."
                                                                                                                                    Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseset@watson.wustl.edu This clone is available royalty-free through Linl.; contact the IMAGE Consortium (info@limage.llnl.gov) for further information. MGI:430469 Seq primer: -28ml3 rev2 ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Marra M., Hillier L., Allen M., Bowles M., Dietrich N.,
Dubuque T., Geisel S., Kucaba T., Lacy M., Le M., Martin J.,
Morris M., Schellenberg K., Steptoe M., Tan F., Underwood K.,
Moore B., Theising B., Wylie T., Lennon G., Soares B., Wilson R.,
                                                                                                                                                                                                                                                            13-FEB-1997 (Rel. 50, Created)
13-FEB-1997 (Rel. 50, Last updated, Version 1)
my25f11.rl Barstead mouse pooled organs MPLRB4 Mus musculus CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_1659999" /clone_11b="Barstead mouse pooled organs MPLRB4"
                                                                                                                                                                                                                                                                                                                                                              Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                264 ccgtccccttctgaacagcaggttgcccaggacacagaggaggtctttcgaagctac
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                                                  Length 320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 39; DB 108; Length 33.
Pred. No. 6.98e-27;
                                                  Score 39; DB 56; Length 320
Pred. No. 6.98e-27;
0; Mismatches 9; Indels
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     64
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/strain="FVB/N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The WashU-HHMI Mouse EST Project";
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                                                                                                                                                                                                                  standard; RNA; EST; 331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="mixed"
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                                                  Query Match 1.9%;
Best Local Similarity 84.2%;
Matches 48; Conservative
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Best Local Similarity 84.2%;
Matches 48; Conservative
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MM1139075
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Marra,M., Hilliar,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theishng,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@lmage.llnl.gov) for further information. MGI:361866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                             185 ctccaccaagacctgaaaaatggcatctggacaaggaccaggtcccccgaagtgggc-tg 243
                                                                                                                                                                           244 cgatgagtc--ccc-gtcc-c--cttctgaacagcaggttgcccaggacacagaggggt 297
                                                                                                                                           AA139013 320 bp mRNA EST 16-FEB-1997 mr04e06.rl Scares mouse 3NbMS Mus musculus cDNA clone 596434 similar to TR:G595926 G595926 BAK-2 PROTEIN.;. g1701240
                                                                                  Gaps
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                7;
                                                  Length 310,
   1 others
                                               Score 40; DB 58; Length 310
Pred. No. 1.60e-28;
0; Mismatches 22; Indels
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/sex="male"
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 55 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism-"Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'tissue_type="Spleen"
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/lab_host="DH10B"
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                                               Query Match 1.9%;
Best Local Similarity 78.2%;
Matches 104; Conservative
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DEFINITION

ACCESSION

KEYWORDS

ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL COMMENT

Parkway

into the

source

FEATURES

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Gaps

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10-FEB-1997

mRNA

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1 (bases 1 to 331)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptce,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    my25f11.rl Barstead mouse pooled organs MPLRB4 Mus musculus cDNA
clone 696909 5'.
AA220617
g1838404
                                                                                                                                                                                                                                                                                                                                                                                                                WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseestewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:430469
                                                                                                                                                                    Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: -28ml3 rev2 ET from Amersham.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                Contact: Marra M/Mouse EST Project
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/organism="Mus musculus"
/strain="FVB/N"
                                                                                                                                                                                                                                                                                                                            Waterston, R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="mixed"
/dev_stage="7 day"
/lab_host="DH10B"
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Search completed: Thu Aug 21 11:52:14 1997 Job time : 1336 secs.



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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm

Wed Aug 20 10:59:48 1997; MasPar time 5.42 Seconds 445.716 Million cell updates/sec Run on:

not generated Tabular output >US-08-320-157-7 (1-211) from USO8320157.pep 1561 1 MASGGGPGPPRQECGEPALP......LVVLGVVLLGQFVVRRFFKS 211 Description:

Perfect Score:

Sequence:

PAM 150 Scoring table:

96640 segs, 11439865 residues Searched:

Listing first 45 summaries Minimum Match 0% Post-processing:

Database:

iparti 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 a-geneseq27

scale 0.228 Variance 142.854; Mean 32.533; Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

* Query Match	OI BO	Description
in bengun	2	scription
100.0 211 2	0 W03668 Bak	k protein.
100.0 211 3		Bcl-Y apoptosis-relat
100.0 211 1	L3 R77876 Hum	Human Cdn-1.
98.0 211 3		Bak-2 protein.
98.0 211		Human Cdn-2.
73.9 152		Human Cdn-1(60-211).
69.1 141 1	.3 R77880 Hum	Human Cdn-1(71-211).
57.5 116 1		Human Cdn-1(96-211)
17.6 190 1		
17.4 232 1	_	icken lymphoid BCL-
17.0 233 1		Chicken lymphoid BCL-Apoptosis-blocking pr
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7 232 1	R77881 R68884 W01020 R68887 W05821	Chicken lymphoid BCL- Apoptosis-blocking pr Human thymus BCL-XL. BCl-XL protein.
7 239 3	R77881 R68884 W01020 R68887 W05821	Chicken lymphoid BCL- Apoptosis-blocking pr Human thymus BCL-XL. BCl-XL protein.
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16.6 239 1	RA77881 R68884 W01020 R68887 W01019 W01019 R71405 R71405	Chicken lymphoid BCL-Apoptosis-blocking pr Human thymus BCL-XL. BCL-XL protein. Apoptosis-blocking pr Apoptosis-blocking pr Human bCl-2 beta prot Human bCl-2 protein.
9	RA77881 R68884 W0108820 R68837 W01019 W11018 R71405 R71405 R71404	Chicken lymphoid BCL. Apoptosis-blocking pr Hunan thymus BCL-XL. BCL-XL protein. Apoptosis-blocking pr Apoptosis-blocking pr Apoptosis-blocking pr Hunan bCl-2 beta prot Human bCl-2 protein. Human bCl-2 protein.
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Human bcl-2 protein. Bcl-2 oncogene produc Sequence of pcl-2-bet	Apoptosis-blocking pr Murine Bax protein.	Human Cdn-3. Human Bax protein.	Human mcl-1 gene prod Human thymus BCL-X1.	Deduced sequence enco Human thymus BCL-XS.	fy blood group g	ACT-4-h-1 receptor se ACT-4 cell surface re	<b>J</b> ,	Insecticidal protoxin Peripheral nervous sy	Peripheral nervous sy	rassa mtr gene	Mrr protein of Neuros Inositol-3-phosphate	Full-length receptor-	Mature non-differenti	Full length receptor-	Human non-differentia
R70331 R42312 P80988	W01021 R71407	R77878 R71406	R68814 R68885	R76996 R68888	R73955	R79904 R74737	R79163	R48678 R99639	R92317	R79909	R13887	W06331		633	R89263
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## ALIGNMENTS

Disclosure; Fig 1; 24pp; English.

Interacts with Epstein-Barr virus (EBV) early lytic cycle BHRF1

protein, and is capable of modulating apoptosis. The protein may

be used in complete or partial form, or as an epitope tag fusion

protein, in a new virucide drug screening method, which involves

combination of Bak protein and a viral protein (e.g. BBV BHRF1),

Exposure to a test compound, and monitoring for disruption of the

interaction, e.g. by co-precipitation, protein interactive trapping

or ELISA. Interaction of Bak and viral proteins allows viral

replication or latency in the absence of apoptosis. Compounds which

inhibit the interaction may be used as virucide, antitumour or

diagnostic agents. Compounds which Human; Bak; apoptosis; latency; virus replication; Epstein-Barr virus; BHRF1; fusion protein; epitope tag; drug screening; co-precipitation; ELISA; immunoassay; antibody; protein interactive trapping; virucide; antitumour; diagnostic. Screening for anti-viral agents - by detecting the ability of agent to disrupt the interaction of a Bak protein and a viral standard; Protein; 211 AA. 24-OCT-1996; 19-APR-1996; UO5639. 20-APR-1995; US-426529. (LXRB-) LXR BIOTECHNOLOGY INC. 22-FEB-1997 (first entry) Kiefer MC; Barr PJ, Kiefer M WPI; 96-485886/48. N-PSDB; T42138 Homo sapiens. WO9633416-A1. Bak protein. T W03668 RESULT DOWN WENT THE PROPERTY OF THE

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ö Length 211; Indels Score 1561; DB 20; Pred. No. 5.68e-137; 0; Mismatches 0; Similarity 100.0%; Similarity 100.0%; 211; Conservative Query Match Best Local Simil Matches 211;

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Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV;
autoimmune disease; reperfusion injury; hepatitis, osteoporosis;
                                                                                                                         30-NOV-1994; U13930.
30-NOV-1994; U2-160067.
07-007-1994, US-320157.
(LARB-) LAR BIOTECHNOLOGY INC.
WPI: 95-211506/28.
N-PSDB; Q95492.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Screening for anti-viral agents
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20-APR-1995; US-426529.
(LXRB-) LXR BIOTECHNOLOGY INC
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100.0%;
Best Local Similarity 100.0%;
Matches 211; Conservative
   (first entry)
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                                                                  shock; lymphoma; eczema
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WO9633416-A1.
                                                                                 Homo sapiens.
W09515084-A.
   21-NOV-1995
                Human Cdn-1
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                                                                                                               08-JUN-1995
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                                                               9ginwgrvvallgfgyrlalhvyqhgltgflgqvtrfvvdfmlhhciarwiaqrggwvaa 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 96-139648/14.
NP-PSDB; T17375.
New isolated human Bcl-Y protein - used to develop prods. for
treating disorders characterised by inappropriate cell proliferation
or coll death.
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Claim 3: Fig 4: 100pp; English.

Bel-Y protein (R81451) is a member of the Bel-2 family and can had easy a protein (R81451) is a member of the Bel-2 family and can induce apoptosis in celis and function as a negative regulator of Bel-2 function. Bel-Y mRNA was detected in all human tumour cell inses examined and is also widely expressed in primary human tissues. It can be obte, by expression of a full-length CDNA clone (T1775) in pref. mammalian host cells. Bel-Y can be used to develop profes. For treating disorders associated with inappropriate cell proliferation or cell death, and to raise antibodies used for the diagnosis or monitoring of such disorders.
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                                                                                                                                                                                                                                                   02-JUL-1996 (first entry)
BCl-Y apoptosis-related protein.
BCl-Y; apoptosis; cell proliferation; cell death; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 100.0%; Score 1561; DB 17; Length 211; Local Similarity 100.0%; Pred. No. 5.68e-137; nos 211; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                         Jabel. C-terminal_domain
/label. C-terminal_domain
/note= "putative membrane localisation sequence"
22.ppn=10.2
                                                                                                                        181 lnlgngpilnvlvvlgvvllgqfvvrrffks 211
                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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R77876 standard; Protein; 211 AA.
R77876;
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R81451 standard, Protein, 211 AA
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09-AUG-1994; U10103.
09-AUG-1994; US-287427.
11-CCT-1994; US-321071.
(IMMU-) IMMUNOGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              211 AA;
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121 sginwgrvvallgfgyrlalhvyqhgltgflggvtrfvvdfmlhhciarwiagrggwvaa 180
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New nucleic acid sequences encoding Cdn apoptosis modulators - and related vectors, transformed cells, proteins and antibodies, useful or diagnosis and treatment e.g. of HIV infection, reperfusion injury
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                                                                                                                                                          Disclosure; Fig. 3A-B; 66pp; English.

Cdn-1 cDNA was isolated from a human heart cDNA library using a previously isolated clone as probe. Recombinant Cdn-1 was produced in Sf9 and human colon adenocarcinoma HT29 cells. Expression of Cdn-1 in WI-12 lymphoblastoid cells resulted in increased cell survival in response to anti-Fas-mediated apoptosis.
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This Bak-2 protein sequence represents a bcl-1 homologue which interacts with Epstein-Barr virus (EBW) early lytic cycle BHRF1 protein, and is capable of modulating apoptosis. The protein may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; Bak 2; apoptosis; latency; virus replication;
Epstein-Barr virus; BHRF1; fusion protein; epitope tag;
drug screening; co-precipitation; ELISA; immunoassay; antibody;
protein interactive trapping; virucide; antitumour; diagnostic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1561; DB 13; Length 211;
Pred. No. 5.68e-137;
0; Mismatches 0; Indels 0
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181

61 121

Matches

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21-NOV-1995 (first entry)
                                                                                                                                                                                                                                                                               (first entry)
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WPI; 95-215106/28.
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WPI; 95-215106/28.
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WO9515084-A.
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R77879;
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be used in complete or partial form, or as an epitope tag fusion protein, in a new virucide drug screening method, which involves combination of Bak-2 protein and a viral protein (e.g. EBV BRRPI), exposure to a test compound, and monitoring for disruption of the interaction, e.g. by co-precipitation, protein interactive trapping or ELISA. Interaction of Bak-2 and viral proteins allows viral replication or latency in the absence of apoptosis. Compounds which inhibit the interaction may be used as virucide, antitumour or
                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                         New nucleic acid sequences encoding Cdn apoptosis modulators - and related vectors, transformed cells, proteins and antibodies, useful or diagnosis and treatment e.g. of HIV infection, reperfusion injury
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Cdn-2 cDNA was isold. from a human placental genomic library using a 950 bp fragment of Cdn-1 cDNA. Expression of Cdn-2 in mouse progenitor B-cell FL5.12 cells decreased IL-3-induced apoptosis. The Cdn-2 protein displayed 97% amino acid identity with Cdn-1 (R77876).

Sequence 211 AA;
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                                                                                                                                                                                                                               / Match 98.0%; Score 1529; DB 20; Local Similarity 97.2%; Pred. No. 7.28e-134; hes 205; Conservative 5; Mismatches 1;
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Local Similarity 97.2%; Pred. No. 7.28e-134;
les 205; Conservative 5; Mismatches 1;
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R77877 standard; Protein; 211 AA.
R77877;
21-NOV-1995 (first entry)
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30-NOV-1994; U13930.
30-NOV-1993; US-160067.
07-OCT-1994; US-320157.
(LXRB-) LXR BIOTECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barr PJ, Kiefer MC;
WPI; 95-215106/28.
N-PSDB; Q95493.
                                                                                                                                                                     diagnostic agents
Sequence 211 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
WO9515084-A.
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New nucleic acid sequences encoding Cdn apoptosis modulators - and related vectors, transformed cells, proteins and antibodies, useful or diagnosis and treatment e.g. of HIV infection, reperfusion injury
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Expression of Cdn-1 in WI-L2 lymphoblastoid cells resulted in increased cell survival in response to anti-Fas-mediated apoptosis. Deletion of the N-terminal 59 amino acids of Cdn-1 only slightly decreased this activity, suggesting that small, truncated Cdn-1 sequence 152 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 mvtlplqpsstmgqvgrqlai1gddinrrydsefqtmlqhlqptaenayeyftkiatslf
                                                                                                                                                                                                                                                                                                                                       Human cdn-1(60-211).
Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV;
autoimmune disease; reperfusion injury; hepatitis, osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV;
autoimmune disease; reperfusion injury; hepatitis, osteoporosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 lnlgngpilnvlvvlgvvllggfvvrrffks 211
                                                                                                                                                           211
                                                                                                                                     181 LNLGNGPILNVLVVLGVVLLGQFVVRRFFKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R77880 standard; Protein; 141 AA
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30-NOV-1993; US-160067.
07-NOV-1994; US-320157.
(LXRB-) LXR BIOTECHNOLOGY INC.
                                                                                                                                                                                                                                                                   standard; Protein; 152
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30-NOV-1993; US-160067.
07-OCT-1994; US-320157.
(LARB-) LXR BIOTECHNOLOGY INC
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Boise LH, Nunez G, Thompson CB; WPI; 95-052079/07.
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Best Local Similarity 28.2%;
Matches 37; Conservative
                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-MAR-1996; 104542.
21-MAR-1995; US-408095.
(UYSL-) UNIV ST LOUIS.
                                                                                                                                                  22-JUN-1994; U07089.
22-JUN-1993; US-081448.
                                                                                                                                                                               (ARCH-) ARCH DEV CORP
(UNMI ) UNIV MICHIGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 qenggwvrtal 189
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172 AQRGGWV-AAL 181
                                                                                                                                                                                                                                                                                                                                                                                                                                       190 AA;
                                                                                                    Gallus domesticus.
                                                                                                                                                                                                                                            N-PSDB; Q81696
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                                                                                                                                                                                                                                                                                                                    71 MGQVGRQLAIIGDDINRRYDSEFQTMLQHLQPTAENAYEYFTKIATSLFESGINWGRVVA 130
                                                                                                                                                                                                                                                       mgqvgrqlaligddinrrydsefqtmlqhlqptaenayeyftkiatslfesginwgrvva 60
New nucleic acid sequences encoding Cdn apoptosis modulators - and related vectors, transformed cells, proteins and antibodies, useful or diagnosis and treatment e.g. of HIV infection, reperfusion injury
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid sequences encoding Cdn apoptosis modulators - and related vectors, transformed cells, proteins and antibodies, useful or diagnosis and treatment e.g. of HIV infection, reperfusion injury
                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                              Disclosure; Fig.11; 66pp; English.

Expression of Cdn-1 in WI-L2 lymphoblastoid cells resulted in increased cell survival in response to anti-Fas-mediated apoptosis. Deletion of the N-terminal 70 amino acids of Cdn-1 improved this activity, suggesting that small, truncated Cdn-1 molecules may be potent therapeutics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig.11; 66pp; English.

Expression of Cdn-1 in WI-L2 lymphoblastoid cells resulted in Expression of Cdn-1 in WI-L2 lymphoblastoid cells resulted in Tarcassed cell survival in response to anti-Fas-mediated apoptosis. Truncated Cdn-1 derivatives given in R77879-81 were used to test the effects of deleting the N-terminal sequences of Cdn-1 on this activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human Cdn-1(96-211).

Human Cdn-1(96-211).

Human Cdn-1; adoptiosis modulator; adoptive immunotherapy; therapy; HIV autoimmune disease; reperfusion injury; hepatitis, osteoporosis; shock; lymphoma; eczema.

Homo sapiens.

W09515084-A.

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Pred. No. 2.53e-90;
0; Mismatches 0; Indels 0
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Pred. No. 6.25e-73;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R68884 standard; Protein; 190 AA
                                                                                                                                                                                                                                                                                                                                                                                    121 vlvvlgvvllgqfvvrrffks 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-NOV-1994; U13930.
30-NOV-1993; US-160067.
07-CCT-1994; US-320157.
(LXRB-) LXR BIOTECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                  191 VLVVLGVVLLGQFVVRRFFKS 211
                                                                                                                                                                                           Query Match
Bost Local Similarity 100.0%;
Matches 141; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%;
Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kiefer MC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barr PJ, Kiefer M
WPI, 95-215106/28.
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                                                                                                                                                               141 AA
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RESULT A

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New poly-nucleotide encoding new poly-peptide(s) that modify apoptosis - and related vectors, recombinant cells and antibodies, useful in assay and for control of cell death in e.g. neuronal cells, lymphocytes and cancers.

Claim 4: Page 87: 127pp: English.

This protein may be expressed recombinantly, particularly with pcmV plasmids as vectors for expression in mammalian cell cultures.

The protein has particular application in cancer cells (failure of programmed cell death (PCD)) or neurodegenerative and autoimmune diseases (premature PCD), e.g. Parkinson's disease, amylotrophic lateral 7 60 vvngatvhrsslevheivrasdvrgalrdagdefelryrrafsdltsglhitpgtaygsf 119 120 eqvvnelfhdgvnwgrivaffsfggalcvesvdkemrvlvgrivswmttyltdh-ldpwi 178 52 VAAPADPEMVTLPLQPSSTMGQVGRQLAIIGDDINRRYDSEFQTMLQHLQPTAENAYEYF 111 Gaps Chicken lymphoid BCL-X.
Chicken; bird; fowl; BCL-X; apoptosis; cell death; cancer;
Chicken; bird; fowl; BCL-X; apoptosis; cell death; cancer;
neurodegenerative disease; autoimnune disease; parkinson; s disease; Commodutar v;
WhPI; 96-427055/43.

Nucleic acids encoding apoptosis regulating proteins - useful for diagnosing and treating immune disorders, malignancies, etc.
Example 8; Pages 34-35; 60pp; English.
The 80-6 mutant (W01020) of the bcl-2 oncogene product (W01018) lacks amino acids 80-86 of the native protein. This and other Bcl-2 mutants (see also W01019-21) were used in a two hybrid assay to examine the interactions between Bcl-2 and novel apoptosis-regulating proteins Nipl, Nip2 and Nip3 (W00997-99). 2 Motifs (W01003-04) on Bcl-2 were identified that are essential for interaction with the Nip proteins. These motifs show homology W01020 standard; Protein; 232 AA.
W01020.
18-DEC-1996 (first entry)
Apoptosis-blocking protein Bcl-2 mutant 80-6 (del80-86).
Apoptosis-regulating protein; Bcl-2; oncogene; adenovirus BlB 19% protein; cell death; cancer; tumour; immune disorder; diagnosis; therapy; BlplA; Blpl3; Blp5; NIP1; 'n amylotrophic lateral sclerosis; multiple sclerosis; oncogene. Length 190 Indels Score 274; DB 13; Le Pred. No. 1.74e-14; 33; Mismatches 59;

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Best Loca Matches

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61 dspavngatghs-ssldarevipmaavkqalreagdefelryrrafsdltsglhitpgta 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BC1-XL protein.

Human; bc1-XL; T-lymphocyte; cell death; BH1 domain; BH2 domain;
BC1-2 homology domain; gene therapy; HIV; AIDS; antisense;
immune discorder; autoimmune disease; graft rejection;
graft-versus-host disease; apoptosis; adoptive immunotherapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          down-regulate the immune response in a T-lymphocyte population
Sequence 233 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-102-1996 (first entry)
Apoptosis-blocking protein Bcl-2 mutant 42-8 (del42-48).
Apoptosis-regulating protein; Bcl-2; oncogene; adenovirus BlB 19% protein; cell death; cancer; tumour; immune disorder; diagnosis; therapy; Blpla; Bipl3; Bip5; NIP1;
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Pred. No. 8.94e-14;
42; Mismatches 60; Indels
                                                                                                                                                    Location/Qualifiers 129..148
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25.5%;
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les 36; Conservative
                                                                                                                                                                                                                          180..191
                                                                                                                                                                                                                                                                                                             02-MAY-1996; U06203.
04-MAY-1995; US-435518.
04-MAY-1995; US-435518.
(ARCH-) ARCH DEV CORP.
(USNA ) US SEC OF NAVY.
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(UYSL-) UNIV ST LOUIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thompson CB;
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21-MAR-1996; 104542.
                                                                                                                                                                                                                                                 "BH2 domain"
                                                                                                                                                                                                  /note= "BH1 domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                    June CH, Thompson WPI; 96-506159/50.
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                                                                                                                               Homo sapiens.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BCL-XL; apoptosis; cell death; cancer; neurodegenerative disease; autoimmune disease; Parkinson disease; amylotrophic lateral sclerosis;
                                                                                                                                                                                                48 ffssqpghtphp-aasrdpvartsplqtpaapgspvppvvhltlrqagddfsrryrrdfa 106
                                                                                                                                                                                                                                                                                             61 dspavngatghs-ssldarevipmaavkqalreagdefelryrrafsdltsglhitpgta 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 yqsfeqvvnelfrdgvnwgrivaffsfggalcvesvdkemqvlvsriaawmatylndh-l 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95 TMLOHLOPTAENAYEYFTKIATSLFESGINWGRVVALLGFGYRLALHVYQHGLTGFLGQV 154
                                                                                                                                                                                                                               New poly-nucleotide encoding new poly-peptide(s) that modify apoptosis - and related vectors, recombinant cells and antibodies, useful in assay and for control of cell death in e.g. claim 3; page 94; 127pp; English.

This protein may be expressed recombinantly, particularly with pcmV plasmids as vectors for expression in mammalian cells cultures. The protein has particular application in cancer cells (failure of programmed cell death (PCD)) or neurodegenerative and autoimmune diseases (premature PCD), e.g. Parkinson's disease, amylotrophic sequence 233 AA;
                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Gaps
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Pred. No. 8.94e-14;
42; Mismatches 60; Indels 3
to motifs (W01005-06) identified on the adenovirus E1B 19K apoptosis-blocking protein (W01010).
                                                                                                  Length 232
                                                                                             Score 272; DB 19;
Pred. No. 2.62e-14;
41; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                               : ::::: | : | | : | | | ::| | | : | | 15 TRFVVDFMLHHCIARWIAQRGGWVAALNLGNGPILNVL 192
                                                                                                                                                                                                                                                                                                                                                                                           167 alwmteylnrh-lhtwiqdnggwdafvel-ygpsmrpl 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Boise LH, Nunez G, Thompson CB;
WPI; 95-052079/07.
N-PSDB; Q81698.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T 11
R68887 standard; Protein; 233 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W05821 standard; Protein; 233 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 epwiqenggwdtfvelygnna 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      168 ARWIAQRGGWVAALNL-GNGP 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              y Match 17.0%;
Local Similarity 25.5%;
hes 36; Conservative
                                                                                             17.4%;
Local Similarity 29.7%;
Les 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W05821;
30-MAR-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-AUG-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-JUN-1994; U07089.
22-JUN-1993; US-081448.
(ARCH-) ARCH DEV CORP.
(UNMI ) UNIV MICHIGAN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
WO9500642-A.
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                                                                                                  Query Match
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Best Loc Matches

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Best Local Similarity
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                       diagnosing and treating improcase registrating functions.

Example 8; Page 33-34; 60pp; English.

The 42-8 mutant (W01019) of the bcl-2 oncogene product (W01018)
lacks amino acids 42-48 of the native protein. This and other
Bcl-2 mutants (see also W01020-21) were used in a two hybrid assay
to examine the interactions between Bcl-2 and novel apoptosis-
regulating proteins Wipl, Wip2 and Nip3 (W00997-99). The Nip
proteins were unable to interact with mutant 42-8. The site of
deletion in this mutant corresponds to a motif (see also W01003)
on Bcl-2 essential for interaction with Nip proteins. A second
binding motif (W01004) of Bcl-2 was also identified, and both
sequence 232 AA;
                                                                                                                                                                                                                           125 tvveelfrdgvnwgrivaffefggvmcvesvnremsplvdnialwmteylnrh-lhtwig 183
                                                                                                                                                                                                                                     tpaapgaaagpalspvppvvhlt--lrqagddfsrryrrdfaemssqlhltpftargcfa 124
                                                                                                                                                                                                          54 APADPEMVTLP-LOPSSTMGOVGROLAIIGDDINRRYDSEFQTMLQHLQPTAENAYEYFT 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                   - useful for
                                                                                                                                                                                                                                                                                                                                        Apoptosis-blocking protein Bcl-2,
Apoptosis-regulating protein; Bcl-2; oncogene;
adenovirus ElB 19K protein; cell death; cancer; tumour;
immune disorder; diagnosis; therapy; Bipla; Bipl3; Bip5; NIp1;
                                                                                                                                                                          ď.
                                                                                                                                                        Score 261; DB 19; Length 232;
Pred. No. 2.48e-13;
37; Mismatches 57; Indels
                   proteins
Chinnadurai G;
WPI; 96-427055/43.
Nucleic acids encoding apoptosis regulating
                                                                                                                                                                                                                                                                                                                                                                                           /label= Binding_motif
/note= "interacts with Bip proteins"
Binding_site 106.112
                                                                                                                                                                                                                                                                                                                                                                                                                                    /label-Binding_motif
/note- "interacts with Bip proteins"
EP-733706-A2.
                                                                                                                                                                                                                                                                                                        /T 14
W01018 standard; Protein; 239 AA.
W01018;
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                                                                                                                                                                                                                                                                       173 QRGGWVAALNLGNGPILNVL 192
                                                                                                                                                      Query Match
Best Local Similarity 29.3%;
Matches 41; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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With year of the producing and identifying mutant bcl-2 proteins -
Wethods for producing and identifying mutant bcl-2 proteins -
Heat lack death repressor activity and/or lacks binding to Bax.

By Disclosure; page 40; 133pp; English.

The sequences given in R71404-05 represent the human bcl-2 alpha and
beta proteins respectively. bcl-2 is encoded by a proto-oncogene and
compared by a proto-oncogene and beta proteins respectively. bcl-2 is encoded by a proto-oncogene and
compared by a proto-oncogene and is capable of inhibiting apoptosis in many hematopoietic cell systems.

Collosing rather than directly promoting proliferation of these cell
corgins rather than directly promoting proliferation of these cell
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corgins rather than directly promoting and consentrations of IL-3. bcl-2 has not been shown to directly promote cell corginal and it
concentrations of IL-3. bcl-2 has bax accelerates apoptotic cell death
collowing an apoptotic stimulus. The invention gives mutant form of
collowing an apoptotic stimulus. The invention gives mutant form
collowing an apoptotic stimulus. This makes the mutant protein substantially
controlling in the BHI or BH2 domains. This makes the mutant protein substantially
controlling in the BH1 or BH2 domains. This makes the mutant protein substantially
controlling an apoptotic cell death represent and diagnosis of immunodeficiency diseases, including AHDS and
controlling and diagnosis of immunodeficiency diseases, including AHDS and
controlling representative and ischaemic cell death.
                                                                                                                                                                                                                                                                                                                       132 tvveelfrdgvnwgrivaffefggvmcvesvnremsplvdnialwmteylnrh-lhtwiq 190
                                                                                                                                                                                                                                                                                                                                                                             74 tpaapgaaagpalspvppvvhlt--irqagddfsrryrrdfaemssgihltpftargcfa 131
                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             apoptosis; membrane-associated cytoplasmic protein; B cell; T cell; proliferation; cell cycle progression; Bax; apoptotic cell death; propiession; BHI; BH2; cancer therapy; hyperplasia; immunodeficiency disease; AIDS; neurodegeneration; ischaemic cell death.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-007-1995 (first entry)
Human bcl-2 beta protein.
Human; bcl-2; alpha; beta; proto-oncogene; hematopoietic cell line;
Human; bcl-2; alpha; beta; proto-oncogene; hematopoietic cell line;
                                                                                           ų,
                Length 239;
    Score 261; DB 19; Length 23
Pred. No. 2.48e-13;
37; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Represents Bax binding site"
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136..155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T 15
R71405 standard; protein; 205 AA.
R71405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     191 dnggwdafvel-ygpsmrpl 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : | | | | :: | | | : | | 13 QRGGWVAALNIGNGPILNVL 192
Query Match
Best Local Similarity 29.3%;
Matches 41; Conservative
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26-AUG-1993; US-112208.
25-MAY-1994; US-248819.
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WPI; 95-106605/14.
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Length 205;

Score 259; DB 13; Pred. No. 3.72e-13;

16.6%;

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Matches 38; Conservative 37; Mismatches 49; Indels 4; Gaps 3;

Db 74 tpaapgaaagpalspyppvvhla--Irqaqddfsrryrgdfaemssqlhltpftargrfa 131

Qy 54 APADPEMVTLP-LQPSSTMGQVGRQLAIIGDDINRRYDSEFQTMLQPLACHTQPTAENAVEYFT 112

Db 132 tvveelfrdgvnwgrivaffefggvmcvesvnremsplvdnialwmteylnrh-lhtwiq 190

113 tlyveelfrdgvnwgrivaffefggvmcvesvnremsplvdnialwmteylnrh-lhtwiq 190

113 tlyveelfrdgvnwgrivaffefgrmcvesvnremsplvdnialwmteylnrh-lhtwiq 190

113 tlyveelfrdgvnwgrivaffefgrmcvesvnremsplvdnialwmteylnrh-lhtwig 190

113 tlyveelfrdgvnwgrivaffefgrmcvesvnremsplvdialwmteylnrh-lhtwig 190

113 tlyveelfrdgvnwgrivaffefgrmcvesvnremsplvdialwmteylnrh-lhtwid 190

114 tlyveelfrdgvnwgrivaffefgrmcvesvnremsplvdialwmteylnrh-lhtwid 190

115 tlyveelfrdgvnwgrivaffefgrmcvesvnremsplvdialwmteylnrh-lhtwid 190

115 tlyveelfrdgvnwgrivaffefgrmcvesvnremsplvdualwmteylnrh-lhtwid 190

115 tlyveelfrdgvnwgr
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Wed Aug 20 11:00:51 1997; MasPar time 8.88 Seconds 686.301 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-320-157-7 (1-211) from USO8320157.pep 1561 1 MASGGGPGPPRQECGEPALF......LVVLGVVLLGGFVVRRFFKS 211 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

91006 seqs, 28888923 residues

Searched:

Post-processing:

Minimum Match 0% Listing first 45 summaries

Database:

pir51 1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3 8:unann4 9:unann5 10:unann6 11:unann7 12:unann8 13:unann9 14:unann10 15:unenc 16:unrev

Mean 45.149; Variance 108.206; scale 0.417 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	NO.	-244	-238	-24	-23	-23	-23	-22	-22	-22	-22	-21	-21	-21	-20	-20	-20	-20	-19	-15	-14	-13
	Pred.	4.946-244	2.15e-238	3.11e-2	1.27e-2	1.27e-2	5.19e-2	1.49e-2	2.11e-2	2.99e-2	6.01e-2	2.436-2	2.43e-	6.88e-2	1.38e-20	1.38e-20	1.38e-20	3.89e-20	6.14e-	1.09e-	4.28e-14	2.24e-13
	Description	Bak protein - human			BCL-X protein - rat	bcl-x long - mouse	apoptosis requlator	bcl-x transmembrane	transforming protein	transforming protein			•		transforming protein	transforming protein	transforming protein	BCL-2 - rat (fragmen	transforming protein	programmed cell deat	bcl-2-associated pro	
SUMMARIES	ឧ	S58873	S58875	A47537	S51761	149056	B47537	149057	B37332	A37332	TVHUB1	D37332	TVHUA1	167431	TVMSB1	TVMSA1	E37332	167432	524390	D47538	A47538	B47538
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	Length DB	211	211	190	233	233	233	214	216	233	202	206	239	233	199	236	237	236	232	192	192	218
đ	Query Match	100.0	98.0	17.6	17.3	17.3	17.0	16.8	16.8	16.7	16.6	16.3	16.3	16.1	16.0	16.0	16.0	15.8	15.3	13.9	13.2	12.9
	Score	1561	1529	274	270	270	266	263	262	261	259	255	255	252	250	250	250	247	239	217	206	201
	Result No.	н	7	m	4	ς.	9	7	<b>ω</b>	0	10	11	12	13	14	15	16	17	18	19	20	21

#gene GDB:BAK-LSB ##cross-references GDB:635887 SUMMARY #length 211 #molecular-weight 23409 #checksum 801

153355 bax - rat (fragment) 3.00e-11 53395 bax - rat (fragment) 3.00e-11 158921 BAX splice form delt 5.36e-10 14949 benepoletic-specific 7.37e-10 coat protein - straw 6.5e-02 cytochrome-c oxidaw 6.5e-02 cytochrome-c oxidaw 6.5e-02 cytochrome-c oxidaw 6.5e-02 cytochrome-c oxidaw 1.44e-01 S53595 beta-glucosidase - S 4.07e-01 beta-glucosidase - S 4.07e-01 cytochrome-c oxidaw 1.25e-01 cytochrom	ALIGNMENTS  type complete - human g; cdn-1 protein Homo sapiens #common_name man #sequence_revision 01-Mar-1996 #text_change 6 72; S58874	Harrington, E.A.; O'Connor, R.; Flemington, 374:733-736  374:733-736  Tapoptosis by the Bcl-2 homologue Bak.  Try; nucleic acid sequence not shown  Tabel CHI  Tabel CHI  White, J.H.M.; Martinou, I.; Raven, T.; Pun, am, C.J.; Martinou, J.C.; Brown, R.  374:731-733  The contraction with adenovirus ocl-2 homologue by interaction with adenovirus	ary  (84213  Brauer, M.J.; Powers, V.C.; Wu, J.J.; Umansky, L.D.; Barr, P.J.  374:736-739  apoptosis by the widely distributed Bcl-2 ak.  1ry  Label KIE
11.3 350 133 145 111.3 111.3 111.3 111.3 11.3 11.3 11.3	58873 #t av protein - el-2 homolog formal_name 5.Feb-1996 # 6.Feb-1996 88873; SS887	Chittenc Chittenc Nature ( Inductic SS8873 Pre type mre type mre erences SS8873 Pre Tarrow, K.T.;	S58872 e_type preliminary preliminary eferences EMBL:X84, S58874 Kiefer, M.C.; Br. S.R.; Tomei, L. Nature (1995) 37- Modulation of app homologue Bak. S58874 preliminary e_type mRNA s-1-211 ##labu eferences EMBL:U16
22 192 192 192 193 193 193 193 193 193 193 193 193 193	RESULT 1 TITLE ALTERNATE_NAMES ORGANISM DATE	authors authors journal title accession #fstatus #fmolecule #fross-re RENCE authors journal	#accession ##status ##status ##residues ##cross-ref #authors #journal #journal #title #accession #status ##status

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Nature (1995) 374:736-739
Modulation of apoptosis by the widely distributed Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Data
                                                                                                                                                                                                    121 sginwgrvvallgfsyrlalhiyqrgltgflgqvtrfvvdfmlhhciarwiagrggwvaa 180
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apoptosis regulator bcl-x - chicken
#formal_name Gallus gallus #common_name chicken
03-May-1994 #sequence_revision 03-May-1994 #text_change
A47537
A47537
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  Score 1561; DB 13;
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0; Mismatches 0;
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Best Local Similarity 97.2%; Pred. No. 2.15e-238;
Matches 205; Conservative 5; Mismatches 1;
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Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.;
Lindsten, T.; Turka, L.A.; Mao, X.; Nunez, G.; Thompson,
C.B.
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bcl-x, a bcl-2-related gene that functions as a dominant
regulator of apoptotic cell death.
A47537
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BCL-X protein - rat
#formal_name Rattus norvegicus #common_name Norway rat
07-May-1995 #sequence_revision 01-Sep-1995 #text_change
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submitted to the EMBL Data Library, November 1994
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Pred. No. 1.27e-23;
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Pred. No. 3.11e-24;
33; Mismatches 59; Indels
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##cross-references GB:L20120
:X #length 190 #molecular-weight 21467
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Best Local Similarity 25.5%;
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Lindsten, T.; Turka, L.A.; Mao, X.; Nunez, G.; Thompson,
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#Journal J. Immunol. (1994) 153:4388-4398
#title Cloning and molecular characterization of mouse bcl-x in and T lymphocytes.
#cross-references WID:95052604
#accession 149056
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                                                            bcl-x long - mouse
#formal_name Mus musculus #common_name house mouse
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
15-Oct-1996
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#formal_name Homo sapiens #common_name man
16.Aug-1996 #sequence_revision 16-Aug-1996 #text_change
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X #length 233 #molecular-weight 26132 #checksum 5739
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Pred. No. 1.27e-23;
42; Mismatches 60; Indels 3;
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##molecule_type mRNA
##molecule_type mRNA
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apoptosis regulator bcl-xL - human
bcl-2-related protein
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##cross-references GB:L20121; CDS_PID:Q07817
                                          *type complete
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Matches 36; Conservative
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#label MAT\
#product apoptosis regulator bcl-xS #status predicted
#label MA2
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bcl-x transmembrane deleted - mouse
#formal_name Mus musculus #common_name house mouse
02.Jul-1996 #sequence_revision 02-Jul-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #authors Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.
#journal J. Immunol. (1994) 153:4388-4398
#title Cloning and molecular characterization of mouse bcl-x
and T lymphocytes.
#cross-references WIID:95052604
#accession I49057
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##cross-references EMBL:U10102; NID:9506649; CDS_PID:9506650
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                                                                                                                                                                                                                                                                                                          Length 233;
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transforming protein (bcl-2-beta) - chicken
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#length 214 #molecular-weight 23900
                ##residues 1-69,'G',71-125,189-233 ##label ##cross-references GB:L20122; CDS_PID:9623237
                                                                                                                                                                                                                                                                                                      Score 266; DB 13;
Pred. No. 5.19e-23;
                                                                                                       ##cross-references GDB:228079
DS alternative splicing; apoptosis
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Best Local Similarity 25.5%;
Matches 36; Conservative
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##residues 1-214
##molecule_type mRNA
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                                                                                      Eguchi, Y.; Ewert, D.L.; Tsulimoto, Y.
Nucleic Acids Res. (1992) 20:4187-4192
Isolation and characterization of the chicken bcl-2 gene:
expression in a variety of tissues including lymphoid and
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#formal_name Gallus gallus #common_name chicken
03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change
12-Apr-1995 #
#formal_name Gallus gallus #common_name chicken
03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change
15-Jun-1996
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                                                                                                                                                                                                                                                                                                                                                  DB 6; Length 216;
                                                                                                                                                                                                                                                                                                                                              Score 262; DB 6; Length 216
Pred. No. 2.11e-22;
38; Mismatches 56; Indels
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                                                                                                                                                                neuronal organs in adult and embryo.
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transforming protein
*length 233 *molecular-weight 25687
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Best Local Similarity 28.5%;
Matches 39; Conservative
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#authors Tsujimoto, Y.; Croce, C.M.
#journal Proc. Natl. Acad. Sci. U.S.A. (1986) 83:5214-5218
#title Analysis of the structure, transcripts, and protein products
of bcl-2, the gene involved in human follicular lymphoma.
#cross-references MUID:86259760
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#map_position 18q21.33-18q21.33
CLASSIFICATION #superfamily bcl transforming protein
KEYWORDS alternative splicing; B-cell lymphoma; follicular lymphoma;
transforming protein
transforming protein
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Nucleic Acids Res. (1992) 20:4187-4192
Isolation and characterization of the chicken bcl-2 gene:
expression in a variety of tissues including lymphoid and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74 tpaapgaaagpalspvppvvhla--lrqagddfsrryrgdfaemssglhltpftargrfa 131
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                                                                                  TVHUB1 #type complete transforming protein bcl-2-beta - human #formal_name Homo sapiens #common_name man 31-bec-1988 #sequence_revision 31-bec-1988 #text_change 06-Sep-1996
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#superfamily bcl transforming protein
#length 206 #molecular-weight 22440 #checksum 5581
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Pred. No. 2.43e-21;
35; Mismatches 51; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1-205 ##label TSU
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HHCIARWIAQRGGWVAALNL-GNG 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##cross-references GDB:119031
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Best Local Similarity 29.7%;
Matches 38; Conservative
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#journal Cell (1986) 47:19-28
#title Cloning and structural analysis of CDNAs for bcl-2 and a hybrid bcl-2/immunoglobulin transcript resulting from the t #cross-references MUID:87002488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  **authors Tsujimoto, Y.; Croce, C.M. (1986) 83:5214-5218 #*Journal Proc. Natl. Acad. Sci. U.S.A. (1986) 83:5214-5218 #title Analysis of the structure, transcripts, and protein products #cross-references MulD:86259760 #accession A29409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #authors Seto, M.; Jaeger, U.; Hockett, R.D.; Graninger, W.; Bennett, S.; Goldman, P.; Korsmeyer, S.J.
#journal EMBO J. (1988) 7:123-131
#title Alternative promoters and exons, somatic mutation and deregulation of the Bcl-2--Ig fusion gene in lymphoma.
#cross_references MUID:88196071
                                                                                                                                                                                                                                                                                                                                                               Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. (1992) 20.4187-4192
Isolation and characterization of the chicken bcl-2 gene:
expression in a variety of tissues including lymphoid and
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Consequences of the t(14:18) chromosomal translocation in follicular lymphoma: deregulated expression of a chimeric and mutated BCL-2 gene.
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this sequence has been corrected in reference A37332
                                                         133 twveelfrdgvnwgrivaffefggvmcvesvnremsplvdnialwmteylnrh-lhtwig 191
                                                                                                                                                                                                                               TVHUA1 #type complete
transforming protein bol-2, splice form alpha - human
#formal_name Homo sapiens #common_name man
31-bec-1988 #sequence_revision 07-Jun-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid sequence not shown; not compared with conceptual translation
54 APADPEMVILP-LQPSSTMGQVGRQLAIIGDDINRRYDSEFQTMLQHLQPTAENAYEYFT
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##molecule_type mRNA
***~~'fil8-239 ##label
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##residues 1-58,'T',60-239 ##label HUA
cession B27622
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this report is a correction
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Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L. Endocrinology (1995) 136:232-241

Expression of members of the bcl-2 gene family in the immature rat ovary: equine chorionic gonadotropin-mediated inhibition of granulosa cell apoptosis is associated with decreased bax and constitutive bcl-2 and bcl-xlong messenger ribonucleic acid levels.
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                                                                                                                                                                                                                                                                        blocks apoptosis in hematopoietic cells
#superfamily bcl transforming protein
alternative splicing; B-cell lymphoma;
proto-oncogene; transforming protein
#length 239 #molecular-weight 26266 #checksum 8323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83 maavkqalreagdefelryrrafsdltsqlhitpgtvyqsfeqvvnelfrdgvnwgriva 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74 tpaapgaaagpalspvppvvhlt--lrqagddfsrryrrdfaemssglhltpftargrfa 131
sidues 1-6,'S',8-58,'T',60-128,'C',130-239 ##label HUA2 to the sequence was determined from the germine gene Constitutive expression of BCL2 following t(14:18) chromosomal translocation is typically found in follicular lymphoma.
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26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
26-Jul-1996
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transforming protein bcl-2-beta - mouse
fromal_name Mus musculus #common_name house mouse
31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##residues 1.233 ##label RES ##cross-references EMBL:U34963; NID:91004376; CDS_PID:91004377 ##cross-references EMBL:U34963; NID:91004376; CDS_PID:91004377 # Length 233 #molecular-weight 26122 #checksum 8310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 255; DB 2; Length 239
Pred. No. 2.43e-21;
37; Mismatches 57; Indels
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Pred. No. 6.88e-21;
31; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #type complete
                                                                                                                                                                                     ##cross-references GDB:119031
#map_position 18q21.33-18q21.33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  173 ORGGWVAALNLGNGPILNVL 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #cross-references MUID:95129487
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Best Local Similarity 28.4%;
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 16.3%;
Best Local Similarity 29.3%;
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BCL-X-Long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##molecule_type mRNA
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#journal Cell (1987) 49:455-463
#title Molecular analysis of mbcl-2: structure and expression of the murine gene homologous to the human gene involved in follicular lymphoma.
#cross-references MUID:87187643
#accession A25960
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                                                                                                                                                                                                                                                                                                                                                                                                                                   A90893
Negrini, M.; Silini, E.; Kozak, C.; Tsujimoto, Y.; Croce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Negrini, M.; Silini, E.; Kozak, C.; Tsujimoto, Y.; Croce,
                                                                                                                                                                                                                                                                                                                                                                               1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TVMSA1 *type complete transforming protein bcl-2-alpha - mouse transforming protein bcl-2-alpha - mouse *formal_name Mus musculus *common_name house mouse 31-Dec-1988 *sequence_revision 31-Dec-1988 *text_change 02-Jun-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Gaps
                                                                                  #journal Cell (1987) 49:455-463
#title Molecular analysis of mbcl-2: structure and expression mursine gene homologous to the human gene involved in follicular lymphoma.
#colss-references MUID:87187643
                                                                                                                                                                                                                                                                 *superfamily bcl transforming protein alternative splicing; transforming protein *length 199 *molecular-weight 22299 *checksum 7397
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192/3
#superfamily bcl transforming protein
ternative splicing; transforming protein
#length 236 #molecular-weight 26524 #checksum 6709
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Pred. No. 1.38e-20;
29; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 30.4%; Pred. No. 1.38e-20;
Matches 35; Conservative 31; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: Wed Aug 20 11:01:37 1997 Job time: 46 secs.
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**residues 1-236 **label NEG
                                                                                                                                                                                                                1-199 ##label NEG
                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 31.1%;
Matches 32; Conservative
02-Jun-1994
                                                                                                                                                                                            ##molecule_type DNA
                                                                                                                                                                             B25960
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CLASSIFICATION
KEYWORDS
SUMMARY
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CLASSIFICATION
KEYWORDS
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#title
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                                                  #authors
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              ACCESSIONS
REFERENCE
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	p protein - protein database search, using Smith-Waterman algorithm Wed Aug 20 11:01:54 1997; MasPar time 6.20 Seconds 722.269 Million cell updates/sec	SCORE: (1-211) from US08320157.pep Score: 1561 :: 1 MASGQGPGPPRQECGEPALPLVVLGVVLLGQFVVRRFFKS 211 table: PAM 150 Gap 11	: 59021 seqs, 21210388 residues :essing: Minimum Match 0% Listing first 45 summaries	rot34 t1 2:part2 t8 9:part9	: Mean 47.042; Variance 90.6	ed. No. is the number of results predicted by chance to have a preater than or equal to the score of the result being printed, I is derived by analysis of the total score distribution.	n Pred. N	274 17.6 190 1 BCLX_CHICK APOPTOSIS REGULATOR B 3.45e-30 266 17.0 233 1 BCLX_HUMAN APOPTOSIS REGULATOR B 1.95e-29 266 17.0 233 1 BCLZ_CHICK APOPTOSIS REGULATOR B 1.95e-29 261 16.3 205 1 BCLZ_CHICK APOPTOSIS REGULATOR B 1.10e-28 255 16.3 205 1 BCLZ_CHICK APOPTOSIS REGULATOR B 9.46e-28 256 16.0 299 1 BCLZ_HUMAN PROTEIN BCL-2-BETA. 1.24e-26 250 16.0 236 1 BCLZ_MOUSE PROTEIN BCL-2-ALPHA. 1.05e-25 250 16.0 236 1 BCLZ_MOUSE PROTEIN BCL-2-ALPHA. 1.05e-25 248 15.9 236 1 BCLZ_RAT PROTEIN BCL-2 ALPHA. 1.05e-25 218 14.0 192 1 BAXA_MOUSE PROTEIN BCL-2 ALPHA. 2.45e-25 218 14.0 192 1 BAXA_HUMAN APOPTOSIS REGULATOR B 7.31e-17 201 13.2 218 1 BAXB_HUMAN APOPTOSIS REGULATOR B 7.31e-17 212.3 350 6 MCLL_HUMAN APOPTOSIS REGULATOR B 9.65e-18 217 11.3 172 5 BAXA_HUMAN BAX PROTEIN CYTOPLAS 9.88e-13 218 170 3 EAR_ASFE4 APOPTOSIS REGULATOR B 9.67e-07 219 2 BAXA_MOUSE PROTEIN CYTOPLAS 9.88e-13 217 11.3 172 5 BAXA_MOUSE REQULATOR B 7.95e-06 218 179 3 EAR_ASFE4 APOPTOSIS REGULATOR B 7.95e-06 219 2 COXZ_CAEEL CYTOCHROR C OXIDASE 1.19e-02 210 2 255 COXZ_CAEEL CYTOCHROR C OXIDASE 5.64e-02 210 2 255 COXZ_CAEEL CYTOCHRONINE SYNTHASE (E 5.64e-02 210 2 255 COXZ_CAEEL CYTOCHRONINE SYNTHASE (E 5.64e-02
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HXT3_XEAST LK HXT4_YEAST LK HXT4_YEAST LK YADZ_XCHPD HI YADZ_XCHPD HI YADZ_XCHPD HI YADZ_XCHPD HI YADZ_XCHPD HI YADZ_XCHPD HI RXT6_XCHPD AI YEAST FI WALF_HUMAN MI HXT4_YEAST HI HXT7_YEAST HI HXT7_YEAST HI HXT7_YEAST HI HXT6_XEAST HI HXT7_YEAST HI HXT7_XEAST HI HXT7_XEAST HI HXT7_XEAST HI HXT6_XEAST HI HXT7_XEAST HI HXT7_XEAST HI YAGZ_XCGE PI YAGZ_XCHPO NI RPOB_CYAPP DI YAGZ_XCHPO NI TISD_HUMAN TI	ALIGNMENTS	PRT; 190	ED) SEQUENCE UPDATE) ANNOTATION UPDATE	A; VERTEBRATA;	M., POSTEMA (	LATOR OF APOPTOT HEST EXPRESSION	THE BCL-2 FAMILY	; 7874E430	Score 274; DB Pred. No. 3.45e 33; Mismatches	vrgalrdagdefe]   :     :::	VGRQLAIIGDDIN	fggalcvesvdker	e o i Klanda v i Quei		PRT; 233
267 5 206 7 206 7 206 7 206 7 206 7 206 7 207 11 208 204 6 208 208 208 6 208 208 208 208 208 208 208 208 208 208		STANDARD;	00/816; 01-FEB-1995 (REL. 31, CAEATED) 01-FEB-1995 (REL. 31, LAST SEC 01-FEB-1995 (REL. 31, LAST ANN APOPTOSIS REGULATOR BCL-X.	(CHICKEN). TAZOA; CHORDAT	[1] SEQUENCE FROM N.A. MEDLINE; 93364977. BOISE L.H., GONZALEZ-GARCIA M., POSTEMA C. TURKA L.A., MAO X., NUNEZ G., THOMPSON C.E	08(1993). DOMINANT REGU ECIFICITY: HIG	LYMPHOID DEVELOPMENT. SMILARTY: BELONGS TO T. L; Z23110; G510899; L; A47537; A47537. STEE: PS01080; BCL2.	0 AA; 21467 M	17.6%; Similarity 28.2%; 37; Conservative	rsslevheivrasd	MVTLPLQPSSTMGQ	hdgvnwgrivaffs  :    ::	ESGINMGRYVALLG	rtal 189 :   -AAL 181	STANDARD;
222442 22442 22442 22442 22442 22442 22442 22442 22442 23332 23332 23422 2443 24432 24532 24532 24532 24532 24532 24532 24532 24532 24532 24532 24532		T 1 BCLX_CHICK	Q0/816; 01-FEB-1995 () 01-FEB-1995 () 01-FEB-1995 () APOPTOSIS REG	BCL-A: GALLUS GALLUS EUKARYOTA; ME' GALLIFORMES.	[1] SEQUENCE FROM MEDLINE; 9336 BOISE L.H., G	CELL 74:597-6 -!- FUNCTION: -!- TISSUE SP	LYMPHOID -!- SIMILARIT' EMBL; Z23110; PIR; A47537; PROSITE; PS01	SEQUENCE 19	ry Match L Local ches	0	52 VAAPADPE	120 eqvvnelf	<b>v</b>	1/9 genggwyrtal :      :   172 AQRGGWV-AAL	T 2 BCLX_RAT
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SEQUENCE
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MEDLINE; 9336497.

A BOISE L.H., GONZALEZ-CARCIA M., POSTEMA C.E., DING L.,

BOISE L.H., GONZALEZ-CARCIA M., POSTEMA C.E., DING L.,

LINDSTEN T., TURKA L.A., MAO X., NUNEZ G., THOMPSON C.B.;

CELL 74:597-608(1993).

-!- FUNCTION: DOWINANT REGULATOR OF APOPTOTIC CELL DEATH.

-!- FUNCTION: DOWINANT REGULATOR OF PROPTOTIC CELL DEATH.

-!- ALTERNATIVE PRODUCTS: TWO ISOFORMS, BCX-X(L) (SHOWN HERE) AND

BCL-X(S), ARE DERIYED BY ALTERNATIVE SPLICING.

-!- TISSUE SPECIFICITY: BCL-X(S) IS EXPRESSED AT HIGH LEVELS IN CELLS

CHAT UNDERGO A HIGH RATE OF TURNOVER, SUCH AS DEVELOPING

LYMPHOCYTES. IN COMPRAST, BCL-X(L) IS FOUND IN TISSUES CONTAINING

CONTAINING TO THE BCL-2 FAMILY.

EMBL: 223115; G53237; -.

REMBL: 223115; G53237; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ж
;
                                                                                                                                                                                                                                             P SEQUENCE...

A TISSUE-BRAIN;

A MICHAELIDIS T.M.;

A MICHAELIDIS T.M.;

AL SUBMITTED (DEC-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.

C -1- FUNCTION: DOMINHAT REGULATOR OF APOPTOTIC CELL DEATH.

CC -1- ALTERNATIVE PRODUCTS: TWO ISOFORMS, BCX-X(L) (SHOWN HERE) AND CC -1- ALTERNATIVE PRODUCTS: TWO ISOFORMS, BCX-X(L) (SHOWN HERE) AND CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.

DR RMBL; X82537; G607177; --

DR EMBL; X82537; G607177; --

KW APOPTOSIS: ALTERNATIVE SPLICING.

KM APOPTOSIS: ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 dspavngatghs-ssldarevipmaaykgalreagdefelryrrafsdltsglhitpgta 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 yqsfeqvvnelfrdgvnwgrivaffsfggalcvesvdkemqvlvsriaswmatylndh-1 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48 EAEGVAAPADPEMVTLPLQPSSTMGQVGRQLAIIGDDINRRYDSEFQTMLQHLQPTAENA 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Gaps
                                                                                                                                          RATTUS NORVEGICUS (RAT).
EUKARYOTA; METALOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MISSING (IN BCL-X(S)).
G -> A (IN G510901).
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Pred. No. 1.95e-29;
42; Mismatches 60;
                   01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
APOPTOSIS REGULATOR BCL-X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-CCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
APOPTOSIS REGULATOR BCL-X.
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APOPTOSIS; ALTERNATYE SPLICING.
126 188 MIS
CONFLICT 70 G G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            168 ARWIAQRGGWVAALNL-GNGP 187
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Local Similarity 25.5%;
los 36; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HOMO SAPIENS (HUMAN)
                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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Q07817;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 92379084.

CAZALS-HATEM D.L., LOUIE D.C., TANAKA S., REED J.C.;
BIOCHIM. BIOPHYS. ACTA 1132:109-113(1992).

1 FUNCTION: PROLONGS THE SURVIVAL OF HEMATOPOIETIC CELLS IN THE ABSENCE OF REQUIRED GROWTH FACTORS AND ALSO IN THE PRESENCE OF VARAOUS STIMULI INDUCING CELLULAR DEATH. BLOCKS APOPTOSIS. MIGHT FUNCTION IN AN ANTIOXIDANT PATHWAY TO PREVENT APOPTOSIS AT SITES OF FREE RADICAL GENERATION SUCH AS MITOCHONDRIA.

1 SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE

(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 hhrpeppgsaaasevppae-glrpapp-g-vhlalrqagdefsrryqrdfaqmsgqlhlt 116
                                                                                                                                                                                                                         120 yqsfeqvvnelfrdgvnwgrivaffsfggalcvesvdkemqvlvsriaawmatylndh-1 178
                                                                                                                                                                                                                                                            117 pftahgrfvavveelfrdgvnwgrivaffefggvmcvesvnremsplvdniatwmteyln 176
                                                                                                                                     61 dspavngatghs-ssldarevipmaavkqalreagdefelryrrafsdltsqlhitpgta 119
                                                                                                                                                                          48 EAEGVAAPADPEMVTLPLQPSSTMGQVGRQLAIIGDDINRRYDSEFQTMLQHLQPTAENA 107
                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
E -> S (IN REF. 2).
GSAAASEVPPAEGLRP -> ARLLLVRCPRLRGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ς,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 261; DB 1; Length 233;
Pred. No. 9.46e-28;
41; Mismatches 57; Indels
                                            17.0%; Score 266; DB 1; Length 233; 25.5%; Pred. No. 1.10e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES
-!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                             Indels
                                                                                           42; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (IN REF. 2).
H -> T (IN REF. 2).
G -> V (IN REF. 2).
W; 3376502C CRC32;
  26049 MW; 57C67491 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          233 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; SA4390; S24390.
PROSITE; PSO1080; BCL2.
APOPIOSIS; TRANSMEMBRANE; MITOCHONDRION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE, 92375724.
EGUCHI Y., EWERT D.L., TSUJIMOTO Y.;
NUCLEIC ACIDS RES. 20:4187-4192(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                    epwigenggwdtfvelygnna 199
                                                                                                                                                                                                                                                                                                                                                168 ARWIAQRGGWVAALNL-GNGP 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; D11381; G222794; -. EMBL; D11381; G222794; JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25687 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16.7%;
Similarity 28.5%;
41; Conservative
                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APOPTOSIS REGULATOR BCL-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; 211961; G62970; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GALLUS GALLUS (CHICKEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64
82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121
139
139 1
233 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A37332; A37332
PIR; S24390; S24390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 41; Conser
233 AA;
                                                               Best Local Similarity
Matches 36; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GALLIFORMES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       BCL2_CHICK
Q00709;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
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MEDLINE; 91066924.

A HOCKENBER D., WINDEZ G., MILLIMAN C., SCHREIBER R.D., KORSMEYER S.J.;
A HOCKENBER D., WINDEZ G., MILLIMAN C., SCHREIBER R.D., KORSMEYER S.J.;
A HOCKENBER D., WINDEZ G., MILLIMAN C., SCHREIBER R.D., KORSMEYER S.J.;
C -1- FUNCTION: PROLONGS THE SURVIVAL OF HEMATOPOIETIC CELLS IN THE ABSENCE OF REQUIRED GROWTH FACTORS AND ALSO IN THE PRESENCE OF VARIOUS STIMULI INDUCING CELLULAR DEATH. BLOCKS APOPTOSIS. MIGHT FUNCTION IN AN ANTIOXIDANT PATHWAY TO PREVENT APOPTOSIS. MIGHT FUNCTION IN AN ANTIOXIDAN SUCH AS MITOCHONDRIA.

C -1- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE.
C -1- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES.
II CHRONIC LYMPHATIC LEUKEMIAN BY A CHROMSOMAL TRANSLOCATION
C -1- DISEASE: INVOLVED IN WOLLICH INVOLVES BCLZ AND IMMUNOGLOBULIN GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 tvveelfrdgvnwgrivaffefggvmcvesvnremsplvdnialwmteylnrh-lhtwig 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 tpaapgaaagpalspvppvvhlt--lrqagddfsrryrrdfaemssglhltpftargrfa 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALTERNATIVE PRODUCTS: TWO FORMS OF BCL-2: ALPHA, AND BETA, ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THEY ONLY DIFFER AT THEIR C-TERMINAL ENDS.
SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                      HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE: PSOLOBO; BCL2.
PROSITE: PSOLOBORE; APOPTOSIS; ALTERNATIVE SPLICING; MEMBRANE; MITOCHONDRION; CHROMOSOMAL TRANSLOCATION.
SEQUENCE 205 AA; 22311 MW; ED321E5E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 16.3%; Score 255; DB 1; Length 205; Local Similarity 29.7%; Pred. No. 1.24e-26; nes 38; Conservative 35; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE; 86259760
TSUJINOTO Y. CROCE C.M.;
PROC. NATL. ACAD. SCI. U.S.A. 83:5214-5218(1986).
                                                                                                                                                                                 01-MAR-1989 (REL. 10, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
PROTEIN BCL-2-BETA.
                                                                                                                                                      205 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 92375724.
EGUCHI Y., EWERT D.L., TSUJIMOTO Y.;
NUCLEIC ACIDS RES. 20:4187-4192(1992)
                                                                     :| : || : ||| | :||||
164 HHCIARWIAQRGGWVAALNL-GNG 186
                                                   177 rh-lhnwiqdnggwdafvelygns 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M13995; G179369; ALT_SEQ.
PIR; D29409; TVHUB1.
PIR; D37332; D37332.
MIM; 151430; -.
                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                              REVISIONS TO 96 AND 110.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        191 dnggwyga 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           173 QRGGWVAA 180
                                                                                                                                 LT 5
BC2B_HUMAN
P10416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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-1-FUNCTION: PROLONGS THE SURVIVAL OF HEMATOPOIETIC CELLS IN THE ABSENCE OF REQUIRED GROWTH FACTORS AND ALSO IN THE PRESENCE OF VARIOUS STIMULI INDUCING CELLGIAR DEATH. BLOCKS APOPTOSIS. MIGHT FUNCTION IN ANTIOXIDANT PATHWAY TO PREVENT APOPTOSIS AT SITES OF FREE RADICAL GENERATION SUCH AS MITOCHONDRIA.
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE.
-!- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES.
-!- DISEASE: INVOLVED IN FOLLICULAR LYMPHOMA (FL) (ALSO KNOWN AS TYPE II CHRONIC LYMPHATIC LEUKEMIA) BY A CHROMOSOMAL TRANSLOCATION TISSUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74 tpaapgaaagpalspvppvvhlt--lrqagddfsrryrrdfaemssqlhltpftargrfa 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HOCKENBERY D., NUNEZ G., MILLIMAN C., SCHREIBER R.D., KORSMEYER S.J.;
NATURE 348:334-336(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      132 tvveelfrdgvnwgrivaffefggvmcvesvnremsplvdnialwmteylnrh-lhtwig 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- ALTERNATIVE PRODUCTS: TWO FORMS OF BCL-2: ALPHA, AND BETA, ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THEY ONLY DIFFER AT THEIR C-TERMINAL ENDS.
-!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
EMBL; M13994; G179367; ALT_SEQ.
PIRE, A13994; G179371; -...
PIRE, A29409; TVUUBC.
PIRE, C37332; C37332.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS01080; BCL2.
PROTO-ONCOGENE; APOPTOSIS; ALTERNATIVE SPLICING; TRANSMEMBRANE;
MITOCHONDRION; CHROMOSOMAL TRANSLOCATION.
                                                                                                                                EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 255; DB 1; Length 239
Pred. No. 1.24e-26;
37; Mismatches 57; Indels
                                                                                                                                                                                                                             PROC. NATL. ACAD. SCI. U.S.A. 83:5214-5218(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P -> T (IN REF. 3).
S -> R (IN REF. 3).
75084B59 CRC32;
                                         01-MAR-1989 (REL. 10, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
                 239 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                                         MEDLINE; 92375724.
EGUCHI Y., EWERT D.L., TSUJIMOTO Y.;
NUCLEIC ACIDS RES. 20:4187-4192(1992).
               PRT;
                                                                                                                                                                                                                                                                                                                                                                  CLEARY M.L., SMITH S.D., SKLAR J.;
CELL 47:19-28(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    233 PG
59 P
117 S
; 26266 MW;
                                                                                                                                                                                                                                                           REVISIONS TO 96; 110 AND 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 29.3%;
Matches 41; Conservative
                                                                                                                                                                                             MEDLINE; 86259760.
TSUJIMOTO Y., CROCE C.M.;
               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION.
                                                                                                                  HOMO SAPIENS (HUMAN)
                                                                                       PROTEIN BCL-2-ALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239 AA;
                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE; 86259760.
                                                                                                                                                                                                                                                                                                                                                     87002488
                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 91066924
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM
LT 6
BC2A_HUMAN
P10415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIM; 151430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRANSMEM
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 RESULT
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LT 9
BCL2_RAT
P49950;
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                                                                                                                                                        Query Match
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                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                     94 lrragddfsrryrrdfaemssqlhltpftargrfatvveelfrdgvnwgrivaffefggv 153
                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                              MUS MUSCULUS (MOUSE).
EUKARYOTA; METALOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                          EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                        .;
;
                                                                                                                                              NEGRINI M., SILINI E., KOZAK C., TSUJIMOTO Y., CROCE C.M.; CELL 49:455-463(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-BALB/C; TISSUE-LIVER;
MEDLINE; 87187643.
NEGRINI M., SILINI E., KOZAK C., TSUJIMOTO Y., CROCE C.M.;
                                                                                                                                                                                                                                                                                       Score 250; DB 1; Length 199;
Pred. No. 1.05e-25;
29; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                  154 mcvesvnremsplvdnialwmteylnrh-lhtwiqdnggwyga 195
                                                                                                                                                                                                                                                                                                                                                             138 LALHVYQHGLTGFLGQVTRFVVDFMLHHCIARWIAQRGGWVAA 180
                                        BC2B_MOUSE STANDARD; PRT; 199 AA.
P10418;
01-MAR-1989 (REL. 10, CREATED)
01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
PROTEIN BCL-2.
BCL2 OR BCL-2.
                                                                                                                                                                                                                                                                                                                                                                                    HC2A_MGUSE STANDARD; PRT; 236 AA. BC2A_MGUSE, STANDARD; PRT; 236 AA. 01-MAR.1989 (REL. 10, CREATED) (01-ARR-1993 (REL. 25, LAST SEQUENCE UPDATE) (01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE) BCL2 OR BCL-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REVISIONS TO 221-222.
MEDLINE, 92375724.
EGUCHI Y., EWERT D.L., TSUJIMOTO Y.;
      191 dnggwdafvel-ygpsmrpl 209
              : || | | : | || : |
173 QRGGWVAALNLGNGPILNVL 192
                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 31.1%;
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CELL 49:455-463(1987).
                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                       MEDLINE; 87187643
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NUCLEIC ACIDS RES. 20:4187-4192(1992).

- 1- FUNCTION: PROLONGS THE SURVIVAL OF HEMATOPOIETIC CELLS IN THE ABSENCE OF REQUIRED GROWTH FACTORS AND ALSO IN THE PRESENCE OF STRUCTION STRUCTION TO ARRIOUS STIMULI INDUCING CELLULAR DEATH. BLOCKS APOPTOSIS. MIGHT FUNCTION IN AN ANTIOXIDARY TO PREVENT APOPTOSIS AT SITES COP FREE RADICAL GENERATION SUCH AS MITOCHONDRIA.

- 1- SUBCELLULAR LOCATION: MITOCHONDRIA.

- 1- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF ITSSUES.

- 1- ALTERNATIVE PRODUCTS: TWO FORMS OF BCL-2: ALPHA, AND BETA, ARE PRODUCED BY ALTERNATIVE SPICING OF THE SAME GENE. THEY ONLY

- ISMILARITY: BELONGS TO THE BCL-2: FAMILY.

- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.

- SIMILARITY: BLOONGS TO THE BCL-3 FAMILY.

- TRANSMEM 209 230

- SEQUENCE 236 AA; 7ADFE975 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94 lrragddfsrryrrdfaemssqlhltpftargrfatvveelfrdgvnwgrivaffefggv 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENE 140:231-232(1944).

-1- FUNCTION: PROLONGS THE SURVIVAL OF HEMATOPOIETIC CELLS IN THE ABSENCE OF REQUIRED GROWTH FACTORS AND ALSO IN THE PRESENCE OF FOURTIOUS STIMULI INDUCING CELLULAR DEATH. BLOCKS APOPTOSIS. MIGHT FUNCTION IN AN ANTIOXIDANT PATHWAY TO PREVENT APOPTOSIS AT SITES OF FREE RADICAL GENERATION SUCH AS MITOCHONDRIA.
-1- SUBCELLULAR LOCATION: MITOCHONDRIAL, INNER MEMBRANE.
-1- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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-!- ALTERNATIVE PRODUCTS: TWO FORMS OF BCL-2: ALPHA, AND BETA, ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THEY ONLY DIFFER AT THEIR C-TERMINAL ENDS.

-!- SIMILARITY: BELCONGS TO THE BCL-2 FAMILY.

EMBL; L14680; G408947; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           154 mcvesvnremsplvdnialwmteylnrh-lhtwiqdnggwdafvel-ygpsmrpl 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 250; DB 1; Length 236;
Pred. No. 1.05e-25;
31; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 15.9%; Score 248; DB 1; Length 236 Best Local Similarity 27.2%; Pred. No. 2.45e-25; Matches 40; Conservative 43; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26550 MW; 336E6B40 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-1996 (REL. 34, CREATED)
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
BCL2 OR BCL-2 ALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     236 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 94193015.
SATO T., IRIE S., KRAJEWSKI S., REED J.C.;
GENE 140:291-292(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 30.4%;
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUTHERIA; RODENTIA.
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AI Z.N., MILLIMAN C.L., KORSMEYER S.J.; 74:609-619(1993).
                             MEDLINE; 93364978.
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Q07814;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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106 NAYEYFTKIAISLFESGINWGRVVALLGFGYRLALHVYQHGLTGFLGQVTRFVVDFMLHH 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73 nmelgrmiadvdtdspre-vff-rvaadmfadgnfnwgrvvalfyfasklvlkalctkvp 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :: : :|| |: :|| |: ::|| |: |: || |: || |: || |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: :|| |: ::|| |: ::|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: 
                                                                           122 targrfatvveelfrdgvnwgrivaffefggvmcvgsvnremsplvdnialwmteylnrh 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO THE APOPTOSIS REPRESSOR BCL-2.
ALTERNATIVE PRODUCTS: A 21 KD MEMBRANE PROTEIN ALPHA AND THE TWO CYTOPLASMIC PROTEINS BETA AND GAMMA ARE GENERATED BY ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 seqimktgafllqgflqdragrmagetpeltleqppqdastk-klseclrrigdelds-- 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2.
-1- SUBCELLULAR LOCATION: MEMBRANE.
-1- SUMILENTY: BELONGS TO THE BCL-2 FAMILY.
PROSITE; L2472; G388192; -
PROSITE; PSO1080; BCL2.
APOPTOSIS; TRANSMEMBRANE; ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 218; DB 1; Length 192;
Pred. No. 7.08e-20;
50; Mismatches 75; Indels
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01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
APOPTOSIS REGULATOR BAX, MEMBRANE ISOFORM ALPHA.
                                                                                                                                                                                                                                                                                                                                                                                     01-FEE-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
APOPTOSIS REGULATOR BAX, MEMBRANE ISOFORM ALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              192 AA; 21394 MW; BD035304 CRC32;
                                                                                                                                                                                                                                                                                                                                          192 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-C57BL/6 X DBA/2 F1;
MEDLINE; 93364978.

OLTYMI Z.N., MILLIMAN C.L., KORSMEYER S.J.;
CELL 74:609-619(1993).
                                                                                                                                                                               182 -lhtwiqdnggwdafvel-ygpsmrpl 206
                                                                                                                                                                                                                / Match
Local Similarity 25.6%;
les 46; Conservative
                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MUS MUSCULUS (MOUSE)
                                                                                                                                                                                                                                                                                                               LT 10
BAXA_MOUSE
Q07813;
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ID BA
AC OC
OT OT
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DT OT
DE AL
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OC EN EN
CC EN EN
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HOMO SAPIENS (HUMAN). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALLA; EUTHERIA; PRIMATES.

[1] SEQUENCE FROM N.A.

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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        107 AXEXFTKIATSLFESG-INWGRVVALLGFGYRLALHVYQHGLTGFLGQVTRFVVDFMLHH 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47 QEAEGVAAPADPEMVTLPLQPSSTMGOVGRQLAIIGDDINRRYDSEFQTMLQHLQPTAEN 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32 gdragrmggeapelaldpvpgdastkklseclkrigdelds--nmelgrmiaavdtdspr 89
-!- SUBCELLUIAR LOCATION: CYTOPLASMIC.
-!- SUBCELLUIAR LOCATION: CYTOPLASMIC.
-!- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY ALTERNATIVE SPLICING.
-!- SIMILARTY: BELONGS TO THE BCL-2 FAMILY.
-!- SIMILARTY: BELONGS TO THE BCL-2 FAMILY.
-!- BLA1538; B47538.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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CELL 74:609-619(1993).
-!- FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO THE APOPTOSIS REPRESSOR BCL-2.
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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Pred. No. 7.31e-17;
36; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      147 rllgwigdaggwdgllsyfgtptwqtvtifvagvltasltiwk 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : || ::||| : |: || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 
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01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
APOPTOSIS REGULATOR BAX, CYTOFLASMIC ISOFORM BETA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 13.2%; Score 206; DB 1; I Local Similarity 24.5%; Pred. No. 9.65e-18; les 40; Conservative 45; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APOPTOSIS; TRANSMEMBRANE; ALTERNATIVE SPLICING:
TRANSMEM 172 192 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APOPTOSIS, ALTERNATIVE SPLICING.
SEQUENCE 218 AA, 24220 MW; 82B2FF09 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            172 192 POTENTIAL.
192 AA; 21184 MW; B2E6148A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 12.9%;
Best Local Similarity 27.0%;
Matches 37; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS01080; BCL2.
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EUTHERIA; PRIMATES
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Matches
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--- INDUCTION: EXPRESSION INCREASES EARLY DURING PHORBOL-ESTER INDUCED DIFFERENTIATION ALONG THE MONOCYTE/MAGROPHAGE PATHWAY IN WYELOID LEUKEMIA CELL LINES ML-1.
---- SIMILARITY: BELONGS TO THE BCL2 FAMILY.
EMBL: L08246; --; NOT_ANNOTATED_CDS.
PIR; A47476; A4776.
MIM: 159523; --
                                                                                                                                                                                 90 6-vff-rvaadmfadgnfnwgrvvalfyfasklvlkalctkvpelirtimgwtldf-lre 146
                                                                                                                                                                                                                              174 lyrqsleiisrylreqatgakdtkpmgrsgatsrkaletlrrvgdgvqrnhetvfqgmlr 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         234 kldikneddvkslsrvmihvfødgvtnwgrivtlisfgafvakhlktingescleplaes 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |: |: ::: :| |: |: |: |: |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: ||
                                                                                          47 QEAEGVAAPADPEMVTLPLQPSSTMGQVGRQLAIIGDDINRRYDSEFQTMLQHLQPTAEN 106
32 gdragrmggeapelaldpvpqdastkklsecikrigdelds--nmelgrmiaavdtdspr 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KOZOPAS K.M., YANG T., BUCHAN H.L., ZHOU P., CRAIG R.W.;
PROC., NATL. ACAD. SCI. U.S.A. 90:3316-3250(1993).
-1- FUNCTION: INVOLVED IN PROGRAMMING OF DIFFERENTIATION AND
CONCOMITANT MAINTENANCE OF VIABILLITY BUT NOT OF PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MCLI_HUMAN STANDARD; PRT; 350 AA.
007820;
01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
INDUCED MYELOID LEUKEMIA CELL DIFFERENTIATION PROTEIN MCL1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 12.3%; Score 192; DB 6; Length 350; Best Local Similarity 24.3%; Pred. No. 2.70e-15; Matches 34; Conservative 40; Mismatches 63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
10194B64 CRC32;
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01-0cT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0cT-1996 (REL. 34, LAST ANNOTATION UPDATE)
BAX PROTEIN, CYTOPLASMIC ISOFONM DELTA.
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PROSITE; PS01080; BCL2.
APOPTOSIS; TRANSMEMBRANE; DIFFERENTIATION.
227 227 DOTTENTIAL.
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TISSUE-MYELOID LEUKEMIA CELLS;
MEDLINE; 93234528.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  166 CIARWIAQRGGWVAALN 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HOMO SAPIENS (HUMAN)
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P55269;
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SEQUENCE
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                 MEDLINE; 95331797.

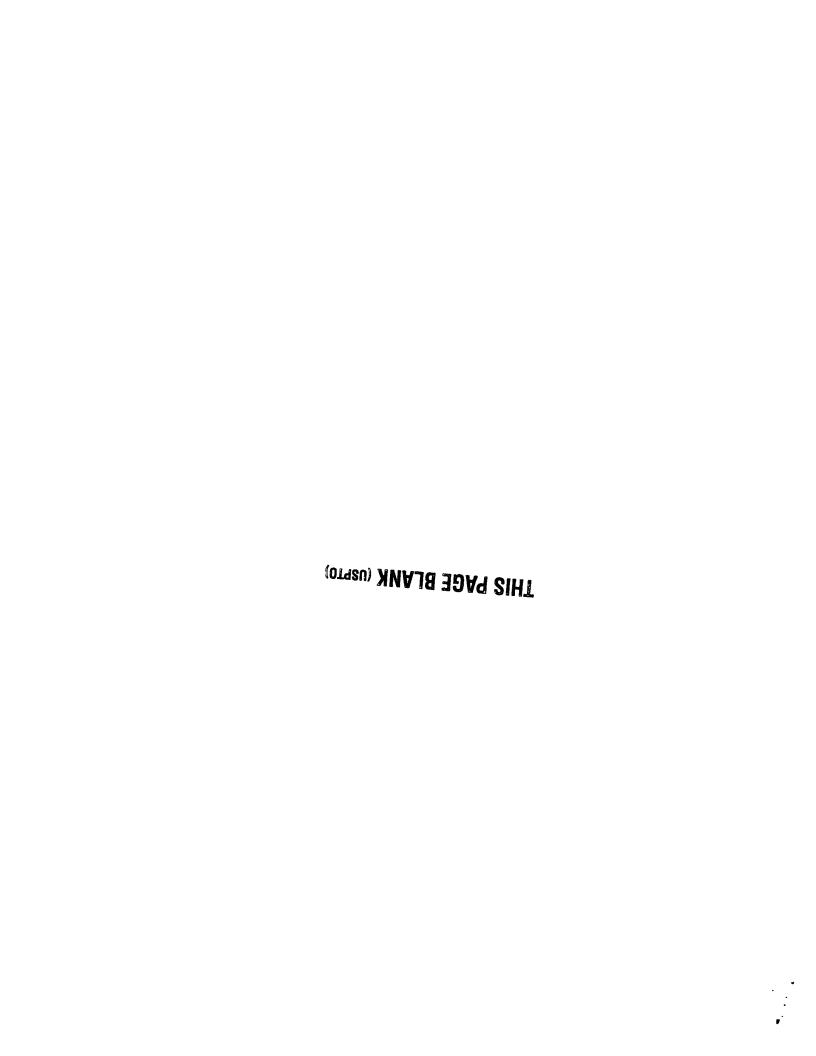
METER S.S., MATTER M.-G., OLSEN B.R.;
GENOMICS 26:592-594(1995).

-I- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY ALTERNATIVE PELICING.

-I- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).

-I- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIN E.Y., ORLOFSKY A., BERGER M.S., PRYSTOWSKY M.B.;
J. IMMUNOL. 151:1979-1988(1993).
-!- FUNCTION: MAY FUNCTION IN THE RESPONSE OF HEMOPOLETIC CELLS TO
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                               Match 11.3%; Score 177; DB 1; Length 143; Local Similarity 27.4%; Pred. No. 9.88e-13; es 29; Conservative 31; Mismatches 43; Indels
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01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
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MIM: 600040; -
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MEDLINE; 93346743.
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Search completed: Wed Aug 20 11:02:15 1997 Job time : 21 secs.



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Release 2.1D John F. Copyright (c) 1993, Distribution	2.1D John F. Collins, Biocomputing Research Unit. t (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.
MPsrch_nn n.a n.	n.a. database search, using Smith-Waterman algorithm
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:10n:	>US-08-320-157-8  -1287) from US08320157.seq
Periect Score: 128/ N.A. Sequence: Comp:	1 TITTAATATATAATTAATGTGCCTCAAGAGTACAGAAGCTT 1287 AAAATTATATTAATTACACGGAGTTCTCATGTCTTCGAA
Scoring table: TABLE Gap 6	default
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Searched: 362067	7 seqs, 549138275 bases x 2
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Databasė: embl- 1:B 9:0	1:BCT 2:FUN 3:GEN1 4:GEN2 5:HTG1 6:HTG2 7:HUM 8:INV 9:OGG 10:MAM 11:VRT 12:PLN 13:FRO 14:ROD 15:SYN 16:UNC
Database: genbank99 18:BCT1 25:BCT8 31:GEN3 38:INV1 52:PEN1 52:PLN1 53:PLN1 54:PR13	14:91K 18:BCT1 19:BCT2 20:BCT3 21:BCT4 22:BCT5 23:BCT6 24:BCT7 25:BCT8 26:BCT9 27:BCT10 28:BCT11 29:GEN1 30:GEN2 31:GEN3 32:HTG1 33:HTG2 34:HTG3 35:INV1 36:GEN2 37:INV3 38:INV4 39:INV5 40:INV6 41:INV7 42:INV8 43:INV9 44:INV10 45:INV11 46:MAM1 47:MAM2 48:MAM3 49:VRT1 50:VRT2 51:VRT3 52:VRT4 53:PAT1 54:PAT2 55:PMT3 56:PAT4 57:PAT5 58:PHG 59:PLN1 60:PLN2 61:PLN3 62:PLN4 63:PLN5 64:PLN5 65:PLN7 66:PLN8 67:PLN9 68:PLN10 69:PLN1 70:PRI 71:PRIS 78:PRIS 78:PRIS 78:PRIS 73:PRIS 78:PRIS 75:PRIS 78:PRIS 78:P
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Database: u-emb150 122:pa	_99 rt1
Statistics: Mean	Mean 11.725; Variance 5.132; scale 2.285

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	0.00e+00	0.00e+00	0.00e+00	0.00e+00	3.97e-149	1.52e-129	4.906-49	1.16e-06	1.44e-01	1.44e-01	1.44e-01	5.48e-01	5.48e-01	5.48e-01	5.48e-01	5.48e-01	5.48e-01	7.12e+00	7.12e+00	2.01e+00	7.12e+00	7.12e+00	7.12e+00	7.12e+00	7.12e+00	2.01e+00 7.12e+00	2.01e+00	7.12e+00	7.12e+00	7.12e+00	7.12e+00	7.12e+00	7.12e+00	7.12			-AUG-1995					A; Homo.	ŭ		2 homologue				LXR
Description	-2 gene, com	sapiens BAK mRNA fo	mkna, compi	Bak-3 pseudogen	DNA sequence **	Human DNA for apotosi	Admin DNA 101 apotosi Segnence 5 from paten	Sequence 5 from paten	Homo sapiens platelet	T.thermophila GB-scRN	X.laevis POMC-A gene	Xenos pecki 285 ribos	Enterococcus faecalis	Leishmania tarentolae	Human DNA sequence fr	Human DNA sequence fr	Human DNA sequence **	M.musculus gast gene	W.suaveolens mitochon	Vesicular scomatitis	Piromyces sp. mRNA fo	D.discoideum CABP1 ge				C.periringens DNA for D.melanogaster fsh me			a r	chromsome 11 97	ce ir	n DNA sequence fr	NA sequence	Human DNA sequence Ir Human BAC clone RG062			PRI 19-AU					yotes; Metazoa; Chordata Catarrhini: Hominidae:	13		widely distributed Bcl-2	. (5			C. Kiefer, Mol. Biol.,
ID						D88396S2	128278	128278	HUMPECAM16	TTGBSCRNA	XLPOMCA	XPU65216	EFU39859	LEIKPMAX	HS162C6	HS162C6	HS3631.9	MMGASTGN3	MTWSORFA	VSVGLYPZ	PSMANC	DDCAMP1	HSE2F1S03	TRBVSGH	CRSTR1	DROFSHA	SOYPHYB	TFLGTFTBPA	CELF55E10		HSCUSUB3 HSSRI.9A1	HS		HSA	ALIGNMENTS		DNA					mitochondrial eukaryo Eutheria: Primates: (	Down	P. G.	osis by the	736-739 (1995	~		994) Michael
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1.6478
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Direct Submission
Submitted (25-JAN-1995) R. Brown, Glaxo Researd
Greenford Road, Greenford, Middlesex UB6 OHE,
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193..828
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human.
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TAENAYEYFTKIATSLFESGINWGRVVALLGFGYRLALHVYQHGLTGFLGQVTRFVVD
FMLHHCIARWIAQRGGWVAALNLGNGPILNVLVVLGVVLLGQFVVRRFFKS"
405 c 400 g 298 t
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                                Length 1360;
                                           Indels
                                             15;
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                              Score 894; DB 73;
Pred. No. 0.00e+00;
0; Mismatches 15
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                              69.5%;
larity 98.2%;
Conservative
                                     Local Similarity
ses 921; Conser
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            257
                                Query Match
            COUNT
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/gene="Bak"
/codon_start=1
/product="Batrotein"
/db_xref="PID:g595924"
/translation="MASGOGEOPPROECGEPALPSASEEQVAQDTEEVFRSYVFYRHQ
QEQAEGVAAPADPEMYLILQPSSTMGQVGROLAIGDDINRRYDSEFQTMLOHLQP
TAENAYESFFRIATSLEESGINWGRVVALLGGFSTRLAHLYCHGLGFFTEGOFTEGOFTEFTUP
FMLHGIARWIAQRGGWVAALNIGNGPILNVLVVLGVVLLGGFVVRRFFKS"
                                                                                                                                                                                                                                                               Mol. Biol., LXR
Richmond, CA 94804, USA
                                                                                                                                                                   Modulation of apoptosis by the widely distributed Bcl-2 homologue
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             19-AUG-1995
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                                                                                     Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2094)
Kiefer,M.C., Brauer,M.J., Powers,V.C., Wu,J.J., Umansky,S.R.
Tomel,L.D. and Barr,P.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      415 GGGCTCCCACTCAGCCCCTGGGAGCAGCAGCCGCCAGCCCCTCGGGACCTCCATCACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tacgttttttaccgccatcagcaggaacaggaggctgaaggggtggctgccctgccgac
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             PRI
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Kiefer,M.C.
Direct Submission
Submitted (02-NOV-1994) Michael C. Kiefer,
Blotechnology Inc., 1401 Marina Way South,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 890; DB 77; I
Pred. No. 0.00e+00;
0; Mismatches 15;
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/organism="Homo sapiens"
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                                                                                                                                                                                Bak
Nature 374 (6524), 736-739 (1995)
95231654
                                                                                                                                                                                                                                                                                                                             /clone="W5"
/clone_lib="WI-L2/ZAP
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/cell_line="EBV t
201..836
      HSU16811 2094 bp m
Human Bak mRNA, complete
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9595923
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ilarity 98.2%;
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      FMLHHCIARWIAQRGGWVAALNLGNGPILNVLVVLGVVLLGQFVVRRFFKS"
1949
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                                                                                                                  1 tgagccacccgggttgggccaggatcccggcaggctgatcccgtcctccactgagacctg
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                                                                   Length
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                                                                 Score 768; DB 77;
Pred. No. 0.00e+00;
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pseudogene,
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Best Local Similarity 98.0%;
Matches 794; Conservative
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/db_xref="PiD:9758798"
/db_xref="PiD:9758798"
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TAENAYEYFRIATSLFESGINWGRVVALLGFGYRLALHYYQHGLTGFLGQVTRFVVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Direct Submission
Submitted (30-MAR-1995) Thomas Chittenden, Apoptosis Technology
Inc., 148 Sidney St., Cambridge, MA 02139, USA
Location/Qualifiers
                                                                                                                                                                                                                          1134
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Chittenden, T., Harrington, E.A., O'Connor, R., Flemington, C., Lutz, R.J., Evan, G.I. and Gullad, B.C.
Induction of apoptosis by the Bcl-2 homologue Bak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/clone_lib="Jurkat cell cDNA library (Stratagene)"
/cell_line="Jurkat cell"
65..700
                                                                                                                                                                                                                                                                                                                            852 tttggggtcccggttcagacccctgcctggacttaagcgaagtctttgccttctctgttcc
   715 CCAGAGATGGTCACCTTACCTCTGCAACCTAGCAGCACCATGGGGCAGGTGGGACGCAG
                                                                                                                             ctgtttgagagtggcatcaattggggccgtgtggtggctcttctgggcttcggctaccgt
                                                                                                                                                895 CTGTTTGAGAGTGGCATCAATTGGGGCCGTGTGGTGGTGGTCTTCTGGGCTTCAGCTACGT
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                                                                                                                                                                                                                                                                                                                                                                                                                            1949 bp mRNA protein mRNA, complete cds.
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Chittenden, T.
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Human Bak E
U23765
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DEFINITION ACCESSION NID

RESULT

KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

TITLE

JOURNAL MEDLINE REFERENCE AUTHORS

TITLE JOURNAL

source

FEATURES

CDS

1079

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19-AUG-1995

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TGGGGCCGTGTGGTGCTCTTCTGGGCTTCAGCTACCGTCTGGCCCTACACATCTACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-MAR-1997 (Rel. 51, Created)
19-MAR-1997 (Rel. 51, Last updated, Version 1)
Human DNA sequence *** SEQUENCING IN PROGRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       contaminates

vith foreign sequence from E.coli, yeast, vec

Order of segments is not known; 800 n's separ

Unfinished sequence: dJ291J10 Contig_ID: 013

Unfinished sequence: dJ291J10 Contig_ID: 015

Unfinished sequence: dJ291J10 Contig_ID: 017

Unfini
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Richmond, CA 94804, USA
                                           1 (bases 1 to 5408)
Kiefer,M.C., Brauer,M.J., Powers,V.C., Wu,J.J., Umansky,S.R.,
Tomel,L.D. and Barr,P.J.
Modulation of apoptosis by the widely distributed Bcl-2 homologue
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 0.00e+00;
0; Mismatches 79; Indels
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y South, P
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Direct Submission
Submitted (02-NOV-1994) Michael C. Ki
Biotechnology Inc., 1401 Marina Way &
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                                                                                                                     Nature 374 (6524), 736-739 (1995)
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CBl(WF. B-mail enquires: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
IMPORTANT: This sequence is unfinished and does not necess:
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| Translation="kuCHLOPTAENAYEYFTKIATSLFESGINWGRVVALLGFGYRLA
| Translation="kuCHLOPTAENAYEYFTKIATSLFESGINWGRVVALLGFGYRLA
LHVYQHGLTGFLGGVTRFVVDFMLHHCIARWIAQRGGWVAALNLGNGPILNVLVVLGV
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Location/Qualifiers
                                                                                                                               Db 107852 gctggcacctctatgatcactggagtctcgcgggtccctcggggctgcacagggacaagta 107911
                                                                                                                                                                                             Db 107912 aaggetacatecagatgeegggaatgeactgaegeeeatteetggaaaetgggeteeeae 107971
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Humen DNA for apotosis-regulator Bak, exon 2, 3 and partial cds.
D88397
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/clone="291J10"
/chromosome="6"
Sequence 123579 BP; 28765 A; 27932 C; 27951 G; 27528 T; 11403 other;
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Eguchi, H. and Hayashi, S.
                                                                                                    Gaps
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 444)
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Estrogen alters expression of apoptosis-regulators, Bcl-2, Bcl-xL and Bak, as well as susceptibility to therapeutic agents of human breast cancer cells Unpublished (1966)

Location/Qualifiers
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                                                                                804 ACGCTATGACTCAGAGTTCCAGACCATGTTGCAGCACCTGCAGCCCACGGCAGAGAATGC 863
                                                         42 tgcccacagcctgtttgagagtggcatcaattggggccgtgtggtggtggctcttctgggctt 101
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                   Gaps
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Submitted (14-OCT-1996) to the DDBJ/EMBL/GenBank databases.
Hidetaka Eguchi, Saitama Cancer Center Research Institute,
Depertment of Biochemistry; 818 Komuro, Ina, Kita-adachi-gun,
Saitama 362, Japan (E-mail:hide@saitama-cc.go.jp,
Tel:048-722-1111(ex.255), Fax:048-722-1739)
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 140)
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Pred. No. 4.96e-49;
0; Mismatches 1;
Pred. No. 1.52e-129;
0; Mismatches 8;
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Homo sapiens
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/clone="pgEMBak01-02"
1..90
/number=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                140 bp
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Best Local Similarity 98.9%;
Matches 89; Conservative
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/number=1
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441 CIGCICCCAGGGGCIGAGIGGGAGC 417
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                                                                                                                                                                                                                           Gaps
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                                                    Dates 1 to 215)
Bennett, A., Labavitch, J.M., Powell, A. and Stotz, H.
Plant inhibitors of fungal polygalacturonases and their use fontrol fungal disease
Patent: US 5569830-A 5 29-OCT-1996;
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Bennett,A., Labavitch,J.M., Powell,A. and Stotz,H.
Plant inhibitors of fungal polygalacturonases and their use
control fungal disease
Patent: US 5569830-A 5 29-OCT-1996;
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Pred. No. 1.16e-06;
85; Mismatches 96; Indels
                                                                                                                                                                                                   57; Length 215;
                                                                                                                                                                 141 others
                                                                                                                                                                                                              Pred. No. 4.92e-08;
71; Mismatches 69; Indels
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8 c 25 q
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Best Local Similarity 11.2%;
Matches 23; Conservative
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Best Local Similarity 16.0%;
Matches 27; Conservative
                                              Unclassified.
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Direct Submission
Submitted (18-DEC-1990) R.L. Hallberg, SYRACUSE UNIVERSITY, BIOLOGY
DEPARTMENT, 130 COLLEGE PLACE, SYRACUSE NY 13244, USA
2 (bases 1 to 1049).
Hallberg, E.M., Fung, P. and Hallberg, R.L.
Genomic sequence encoding a heat shock-induced, RNA polymerase
III-transcribed RNA from Tetrahymena thermophila
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                                                                                                                                                                                                                   Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (basea to 250) Newman, P.J., Berndt, M.C., Gorski, J., White, G.C. II., Lyman, S., Paddock, C. and Muller, W.A. PECAM-1 (CD31) cloning and relation to adhesion molecules of thimmunoglobulin gene superfamily Science 247 (4947), 1219-1222 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   heat shock induced; RNA polymerase III; scRNA.
Tetrahymena thermophila.
Tetrahymena thermophila
Eukaryotae; mitochondrial eukaryotes; Alveolata; Ciliophora;
Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymena.
1 (bases 1 to 1049)
Hallberg, R.L.
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Kirschbaum, N.E., Gumina, R.J. and Newman, P.J.
Organization of the gene for human platelet/endothelial cell
adhesion molecule-1 shows alternatively spliced isoforms and
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Pred. No. 1.44e-01;
0; Mismatches 27; Indels
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platelet endothelial cell adhesion molecule
16 of 27
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Blood 84, 4028-4037 (1994)
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/organism="Homo sapiens"
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<1..>250
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/citation=[2]
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nes 54; Conservative
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QKFDLMYAKRAFVHWYVGEGMEEGEFSBAREDLAALEKDYEEVGIESNBAEGEDEGYE
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/organism="Xenopus laevis"
/clone_lib="lambda EMBL4"
/clone="lambda XPA5"
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1163..1346
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1347..>2525
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Xenopus laevis
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                                                                                                                                                                                                                                                                                                                                                          7. Match 2.1%;
Local Similarity 67.3%;
Les 72; Conservative
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Submitted (27-JUL-1989) Hyde J.E., University of Manchester Institute of Science and Technology, Dept of Biochemistry and Applied Molecular Biology, UMIST P O Box 88, Manchester M60 LQD, UK 2 (bases 1 to 2648)
HOllowary.S.P., Sims, P.F., Delves,C.J., Scaife,J.G. and Hyde,J.E. Isolation of alpha-tubulin genes from the human malaria parasite, Plasmodium falciparum: sequence analysis of alpha-tubulin Microbiol. 3 (11), 1501-1510 (1989)
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malaria parasite.
Plasmodium falotparum
Eukaryotae; mitochondrial eukaryotes; Alveolata; Apicomplexa;
Haemosporida; Plasmodium.
1 (bases 1 to 2648)
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Pred. No. 1.44e-01;
0; Mismatches 23; Indels 1;
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                                                                                                                          /organism="Tetrahymena thermophila"
/strain="BIV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="K1 (Thailand)"
/cell_type="intracrythrocytic"
/clone_lib="lambda NM1149, Hindill"
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/note="proximal sequence element"
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/organism="Plasmodium falciparum"
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/db_xref="SWISS-PROT:P14642"
20 (4), 912 (1992)
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                                                                                                                                                                                                                                                                                                                             447..752
/note="G8-SCRNA"
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Best Local Similarity 70.0%;
Matches 56; Conservative
Nucleic Acids Res.
92178994
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Deen, P.M., Roubos, E.W. and Martens, G.J.
Presence of Vi-transposon-like elements in the prooplomelanocortin gene A of Xenopus laevis does not affect gene activity
Mol. Gen. Genet. 230 (3), 491-493 (1991)
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Vertebrata; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
Pipidae; Xenopodinae; Xenopus.
1 (bases 1 to 9747)
Deen,P.M.T.
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                                                                                                          neuropeptide/opioid; opioid (beta-endorphin); POMC-A gene; preprohormone; proopiomelanocortin-A; repetitive element JH12; repetitive element Vi; secretion.
                                                                                                                                              Gaps
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Deen, P.M.T., Terwel, D., Bussemakers, M.J.M., Roubos, E.W. and Martens, G.J.M.
Comparative analysis of the transcriptionally active Propolomelanocortin genes A and B of Xenopus laevis
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Deen, P.M., Bussemakers, M.J., Terwel, D., Roubos, E.W. and
Martens, G.J.
                                                        ;
Score 27; DB 44; Length 2648; Pred. No. 1.44e-01;
                                                     Indels
                                                                                                                                                                                                                                                            364 taaaaa-taataaaattaaaaaaaaaaaaaaaaagaaaaatttacatatt 409
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X.Laevis POMC-A gene for proopiomelanocortin-A.
X59370 535811
g64988
                                                     0; Mismatches 33;
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Xenos pecki

Eukaryotaes; Metazoa; Arthropoda;

Eukaryotaes; mitochondrial eukaryotes; Metazoa; Arthropoda;

Euracheata: Hexapoda; Insecta; Pterygota; Strepsiptera; Stylopoidea;

Stylopidae; Xeninae; Xenos.

1 (bases 1 to 610)

Whiting, M.F., Carpenter, J.C., Wheeler, Q.D. and Wheeler, W.C.

The Strepsiptera Problem: Phylogeny of the Holometabolous Insect
Orders Inferred From 188 and 288 Ribosomal DNA Sequences and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps 1;
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Whiting,M.F., Carpenter,J.C., Wheeler,Q.D. and Wheeler,W.C.
Direct Submission
Submitted (25-JUL-1996) Entomology, American Museum of Natural
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Pred. No. 1.44e-01;
0; Mismatches 16; Indels 1;
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Xenos pecki 28S ribosomal RNA gene, partial sequence.
U65216
91762761
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539..4905
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4906.5048
/gene="POMC A"
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4306..4590
                                                                                                                    1724..1957
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1972..2459
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                                                                                                                                                                                                                                                                                                                                                                                              /number=2
6886..7347
/note="V1 repetitive element"
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/note="simple sequence"
1 1558 c 1715 g 32
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                                                                                        /gene="POMC A"
/gene="POMC A"
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Best Local Similarity 74.2%;
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17         34         2.6         114         12         070465           19         34         2.6         114         12         070469           20         34         2.6         114         12         070469           21         31         2.4         114         12         070466           23         31         2.4         114         12         070466           24         31         2.4         114         12         070470           25         31         2.4         114         12         070470           26         30         2.3         56         6         035072           27         2.3         10         4         144         2         070470           28         2.2         114         12         070471         2         070471           30         28         2.2         114         12         070471           31         28         2.2         114         12         070471           32         2.2         114         12         070471           33         2.6         2.0         36         0         070471 </th <th>ALIGNMENTS</th> <th>1 42139; 42139; 2-FBB-1997 (first entry) ak-2 gene.</th> <th>Human, Bak.2; apoptosis; latency; viru Epstein-Barr virus; BHRF1; fusion prodrug screening; co-precipitation; ELIS protein interactive trapping; virucide Homo sapiens.  Key  5'UTR  1.543</th> <th>CDS 5441179 /*tag b 5441179 /product= Bak-2 protein 3'UTR 11801286 /*tag c</th> <th>WO9633416-A1. 24-OCT-1996. 19-APR-1995; UO5639. 20-APR-1995; US-426529. (LXRB-) LXR BIOTECHNOLOGY INC.</th> <th>Barr PJ, Kiefer MC; WPI: 96-48586/48. P-PSDB; W03669. Screening for anti-viral agents - by dagent to disrupt the interaction of a protein Disclosure; Fig 2; 24pp; English. The sequence encodes Bak-2 protein, wh interacts with Epstein-Barr virus (EBV protein, and is capable of modulating located on human chromosome-20. The complete or patrial form, or as an epinew virucide drug screening method, wh Bak-2 protein and a viral protein (e.g. by co-precipitation, protein (e.g. by co-precipitation, protein interaction of Bak-2 and viral protein</th>	ALIGNMENTS	1 42139; 42139; 2-FBB-1997 (first entry) ak-2 gene.	Human, Bak.2; apoptosis; latency; viru Epstein-Barr virus; BHRF1; fusion prodrug screening; co-precipitation; ELIS protein interactive trapping; virucide Homo sapiens.  Key  5'UTR  1.543	CDS 5441179 /*tag b 5441179 /product= Bak-2 protein 3'UTR 11801286 /*tag c	WO9633416-A1. 24-OCT-1996. 19-APR-1995; UO5639. 20-APR-1995; US-426529. (LXRB-) LXR BIOTECHNOLOGY INC.	Barr PJ, Kiefer MC; WPI: 96-48586/48. P-PSDB; W03669. Screening for anti-viral agents - by dagent to disrupt the interaction of a protein Disclosure; Fig 2; 24pp; English. The sequence encodes Bak-2 protein, wh interacts with Epstein-Barr virus (EBV protein, and is capable of modulating located on human chromosome-20. The complete or patrial form, or as an epinew virucide drug screening method, wh Bak-2 protein and a viral protein (e.g. by co-precipitation, protein (e.g. by co-precipitation, protein interaction of Bak-2 and viral protein
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######################################	match STD : Dbase	rched: 134151 seqs, 491 L-processing: Minimum Match O%	Database: n-geneseq27 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27	Statistics: Mean 9.436; Variance 5.783; scale 1.632  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES Result Query No. Score Match Length DB ID Description Pred. No.	1 1280 99.5 1286 24 T42139 Bak-2 gene. 2 1269 98.6 6511 14 Q95493 Human Cdn-2 DNA. 0.00e+00 4 889 69.2 2094 24 T42138 Bak gene. 0.00e+00 4 889 69.1 2072 14 Q95492 Human Cdn-1 cDNA. 0.00e+00 5 768 59.7 1968 19 T17375 BcL-Y cDNA. 0.00e+00 6 753 58.5 5408 14 Q95494 Human Cdn-3 DNA. 0.00e+00 7 88 6.8 1047 2 Q10572 Human Natriuretic Pep 5.85e-38 8 77 6.0 1047 2 Q10572 Human Natriuretic Pep 5.42e-31 10 43 3.3 91 9 Q51746 Oligonucleotide probe 1.70e-10 12 40 3.1 204 1 N81164 Base substituted E.co 1.24e-11 14 36 2.8 114 12 Q70466 Generic DNA sequence 1.26e-06 15 35 2.7 114 12 Q70465 Generic DNA sequence 1.26e-06 15 35 2.7 114 12 Q70465 Generic DNA sequence 1.26e-06 15 35 2.7 114 12 Q70465 Generic DNA sequence 4.33e-06

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1.47e-05
4.95e-05
4.95e-05
5.38e-04
5.38e-04
5.38e-04
1.73e-02
1.73e-01
1.7
       Generic DNA sequence
Conjugate formed by 1
Generic DNA sequence
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which is a bcl-1 homologue which (EBV) early lytic cycle BHRF1 ing apoptosis. The Bak-2 gene is he protein may be used in eptrope tag fusion protein, in a which involves combination of (e.g. EBV BHRF1), exposure to a disruption of the interaction, interactive trapping or ELISA. teins allows viral replication or rus replication; otein; epitope tag; ISA; immunoassay; antibody; de; antitumour; diagnostic; ds. an detecting the ability of a Bak protein and a viral

	SUL	FT W09515084-8  PN W09515084-8  DO -JUN-1995.  PF 30-NOV-1994; U13930.  PR 30-NOV-1994; US-160067.  PR (LXRB-) LXR BIOTECHNOLOC PL BAIL PLY KIEGER MC;  DR WPI; 95-215106/28.  PT NOW NUCLEIC SOIG SEQUENCY PT OR DIAGRAMS PT COLLEGE WORLD WORLD PT COLLEGE WORLD WORLD WORLD PT COLLEGE WORLD WORD WORLD WOR	CC using a 950 bp fragment CC in mouse progenitor B-cc CC apoptosis. The GGn-2 pr CC with GGn-1 (R77876). SQ Sequence 6511 BP; 1 Query Match Best Local Similarity 99: Matches 1287; Conservativ Db 2768 ttttaatataaattaatq Db 2828 aattcaaatgtataaqq Db 2828 aattcaaatgtataaqac Db 2888 aqccactgtccatagttt Db 2888 aqccactgtccatagttt CD 2888 agccactgtccatagttt CD 2888 agccactgtccatagttt
later inter Seque Seque best Loc fatches (atches 61 61 121 121	TATTTTTGGTGTATGAACTGTAGTCCTAGAGGATTTTATTAGTTATGAGTTCTATAACT  aggatccatcatcttagttgctaagaacgtagatactgagaacatcatttaaaaaaacat	421 ccactcagccctgggagcagcagcccctcgggacctccatctccacctgct 480	661 ttttaccaccatcagcaggaacaggaagggggggggggg

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perfusion injury; hepatitis, osteoporosis;
a; ss.
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d from a human placental genomic library
t of Cdn-1 cDNA. Expression of Cdn-2
cell FL5.12 cells decreased IL-3-induced
protein displayed 97% amino acid identity
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.8%; Pred. No. 0.00e+00;
ive 0; Mismatches 0; Indels 3;
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Score 890;
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T42138 standard; cDNA; 2094
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Best Local Similarity 98.2%;
Matches 917; Conservative
                                         T42138;
22-FEB-1997 (first entry)
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(LXRB-) LXR BIOTECHNOLOGY
Barr PJ, Kiefer MC;
WPI; 96-485886/48.
                                                                                                                  201..836
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19-APR-1996; U05639.
20-APR-1995; US-4265
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protein.

Disclosure: Fig 1, 24pp; English.

The sequence encodes Bak protein, which is a bcl-1 homologue which interacts with Epstein-Barr virus (EBV) early lytic cycle BHRF1

The rotein, and is capable of modulating apoptosis. The Bak gene is located on human chromosome-6 at 6p21-23. The protein may be used in complete or partial form, or as an epitope tag fusion protein, or an anew virucide drug screening method, which involves combination of Bak protein and a viral protein (e.g. BEV BHRRI), exposure to a test compound, and monitoring for disruption of the interaction, c.g. by co-precipitation, protein interactive trapping or ELISA.

Interaction of Bak and viral protein earlows viral replication or interaction of Bak and viral protein allows viral replication or latency in the absence of apoptosis. Compounds which inhibit the interaction may be used as virucide, antitumour or diagnostic agents.

Sequence 2094 BP; 410 A; 608 C; 606 G; 470 T;
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Human; Bak; apoptosis; latency; virus replication;
Bestein-Barr virus; BHRR1; fusion protein; epitope tag;
drug screening; co-precipitation; ELISA; immunoassay; antibody;
protein interactive trapping; virucide; antitumour; diagnostic; ss.
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Now nucleic acid sequences encoding Cdn apoptosis modulators - and related vectors, transformed cells, proteins and antibodies, useful or diagnosis and treatment e.g. of HIV infection, reperfusion injury
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Gdn-1 cDNA was isolated from a human heart cDNA library using a
proviously isolated clone as probe. Recombinant Cdn-1 was produced
in Sf9 and human colon adenocarcinoma HT29 cells. Expression of
                                                                                                                                                                                             ccagagatggtcaccttacctctgcaacctagcagcaccatggggcaggtgggacggcag
                                                                             ctggccctacacgtctaccagcatggcctgactggcttcctagggccaggtgacccgcttc
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                                                 ctcgccatcatcgggggacgacatcaaccgacgctatgactcagagttccagaccatgttg
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Homo sapiens.
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188..903
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30-NOV-1994; U13930.
30-NOV-1993; US-160067.
07-OCT-1994; US-320157.
(LXRB-) LK BIOTECHNOLOGY INC.
BARY PJ, KIEÉE MC;
WPI; 95-215106/28.
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Q95492 standard; cDNA; 2072
Q95492;
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in response to anti-Fas-mediated apoptosis
2072 BP; 404 A; 603 C; 598 G;
                                                            Score 889; DB 14;
Pred. No. 0.00e+00;
                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ttgcagggtccccctcaagagtacagaagctt
                                                              ch 69.1%;
l Similarity 98.2%;
916; Conservative
                                  Sequence
                                                              Query Match
Best Local S
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Barr PJ, Kiefer MC;
WPI; 95-215106/28.
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                                                                                                                                                                                                                                                                                    Homo sapiens.
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W09515084-A
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                                                                                                                                                                                                          or cell usa.u.
Claim 6; Fig 4; 100pp; English.
A full-length cDNA clone (T17375) codes for Bcl-Y (R81451), a
protein that induces apoptosis in cells and functions as a negative
regulator of Bcl-2 function. It was isolated from a Jurkat cell
cDNA library using as probe a partial Bcl-Y cDNA clone obtd. by
PCR of DNA derived from the Namalwa cell line. The cDNA can be used
for prodn. of recombinant Bcl-Y, as a probe, to produce transgenic
animal models, and in the gene therapy of disorders characterised by
inappropriate cell proliferation or cell death.
Sequence 1968 BP; 382 A; 560 C; 576 G; 450 T;
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                                                                                                                                                                                                                                                                                                                                                                     New isolated human Bcl-Y protein - used to develop prods. for treating disorders characterised by inappropriate cell proliferation or cell death
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ttttaccgccatcagcaggaacaggaggctgaaggggtggctgccctgccgacccaga
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                                                                                                                                                                                                                                                                                                                  'Match 59.7%; Score 768; DB 19; Length 1968; Local Similarity 98.0%; Pred. No. 0.00e+00; les 794; Conservative 0; Mismatches 14; Indels 2
                                              cell death; diagnosis;
                                            Bcl-Y; apoptosis; cell proliferation;
gene therapy; ss.
                                                                        Location/Qualifiers
65..700
           BP.
          standard; cDNA; 1968
                          02-JUL-1996 (first entry)
Bcl-r cDNA.
                                                                                                         22-FEB-1996.
09-AUG-1995; U10103.
09-AUG-1994; US-287427.
11-OCT-1994; US-321071.
(IMMU-) IMMUNOGEN INC.
Chittenden TD;
WPI: 96-139648/14.
                                                                                                                                                                            P-PSDB; R81451.
                                                                                         /*tag= a
WO9605232-A1
                                                               Homo sapiens
RESULT 5
ID T17375 st
AC T17375;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid sequences encoding Cdn apoptosis modulators - and related vectors, transformed cells, proteins and antibodies, useful or diagnosis and treatment e.g. of HIV infection, reperfusion injury
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                    317 ATGATCACTGGAGTCTCGCGGGTCCCTCAGGCTGCACGGGACAAGTAAAGGCTACATCC
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                                                                                                                      1080 AGCCCTGAACTTGGGCAATGGTCCCATCCTGAACGTGCTGGTGGTTCTGGGTGTGTTCT
                                                                                                                                                                                             gttggggccagtttgtggtacgaagattcttcaaatcatgactcccaagggtgccctttgg
                                                                                          601 agccctgaacttgggcaatggtcccatcctgaacgtgctggtggttctgggtgtggttct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig.7A-G; 66pp; English.
Southern Dict analysis of human genomic DNA and a panel of human/rodent somatic cell DNAs revealed at least 3 Cdn-related genes residing on chromosomes 6, 11 and 20. Cdn-3 (R77878) and and contain the structural features of Cdn-1 (R77876), Cdn-2 (R77877) or other Bcl-2 family members.
Sequence 5408 BP; 1369 A; 1384 C; 1314 G; 1341 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cdn-3; apoptosis modulator; adoptive immunotherapy; therapy; HIV
autoimmune disease; reperfusion injury; hepatitis, osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6
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                                                                                                                                                                                                                                                                                                                                                                                          781 aggggtccccctcaagagtacagaagctt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-NOV-1994; U13930.
30-NOV-1993; US-160067.
07-OCT-1994; US-320157.
(LXRB-) LXR BIOTECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP.
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Local Similarity 91.0%;
les 886; Conservative
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Q95494 standard; DNA; 5408
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Human Cdn-3 DNA.
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                1797 aggaacaggaggctgaagggggggggcgccctgccgaccagagatggtcaccttgcccc 1856
                                                                                                                                                            1916 tcaaccggcactatgacttcggagttccagaccatgctgcagcacctgcagccacggca 1975
                                                                                                                                                                                              1976 gagaacgeetacgagtaetteaceaagategeeteeageetgtttgagagtggeateaae 2035
                                                                                                                                                                                                                                                                     2096 cacggettgactggettectgggeetggtgaceegettegtggt---etteatgetgeaa 2152
                                                                                                                                                                                                                                                                                                                                                           1096 AATGGTCCCATCCTGAACGTGCTGGTTCTGGGTGTGGTTCTGTTGGGCCCAGTTTGTG 1155
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                                                                                                 975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human Natriurètic Peptilé Receptor B.
NPRB; ANP; BNP; CNP; kidney failure; heart failure; protein kinase;
hyperaldosteronism; glaucoma; guanyl cyclase.
                                                                                                                                                                                                                                              916 TGGGCCCTGTGGGCTCTTCTGGCTTCAGCTACCGTCTGGCCCTACACATCTACCAG
                                                                                                                                                                                                                                                                                                        2153 caaggcatcgcccggtggatctcgcagaggggcggctgggtggcagccctggacttgggc
497 GCCAGGATCCCGGCTGATCCCGTCCTCCACTGAGACCTGAAAATGGCTTCGGGGC
                                                                                                                        1857 tecaacetageageaceatgggggeaggtgggaeggeagetegeeateaceagg-aegaea
                                                                                                                                                                                                                                  2036 cggggccgtgtggtggctctcctgggcttcggctaccgtctggtcctacatgtctaccag
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                                                                                                                                                                                                                                                                                        976 CGTGGCCTGACTGGCTTCCTGGGCCAGGTGACCCGCTTTGTGGTGGACTTCATGCTGCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Domain 23..455
/label- extracellular domain
/note- "binds natriuretic peptides A,B and C]"
/notel- transmembrane domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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Protein 12
Protein 12
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1227 AAGTCCAGGCAGGCT-CTGAACTGGAACCCCAAAGGCACCCTTGGGAGTCATG-ATTTG 1170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      359 ndgnrnvnkmngrryhgvtgnvvmdknndrntdnvnwamgdndsgdnnnaahysganknn 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  419 wwtgrnnnwykgannsdnnncandnddnscdktnnstnanyangtgntnnmngyssnnnn 478
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The sequence was derived from the DNA encoding natriuretic peptide receptor B, NPRB, having guanyl cyclase (GC) activity and protein kinase activity. The DNA can be inserted into expression vectors for the prodein, opt. after being mutated to produce NPRB analogues. The protein has a mol wt. of 115 kD (calculated Mr-114,952). The protein (or variants) can be used in treatment of natriuretic peptide disorders, and also to isolate peptides using affinity chromatography. Antibodies with affinity for NPRB can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cnrgsnndnnnndsnnndwmnrysnnndnvkgmannhnsnnsshgsnkssncvvdsrnvn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 8.3%; Pred. No. 5.85e-38; es 61; Conservative 215; Mismatches 450; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83 G;
                   /note= "GC and protien kinase activity"
Modified -site 24..26
/label= N-glycos_site
Modified -site 35..37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goeddel D, Lowe D;
'label= cytoplasmic domain
                                                                                                                                                                                                                                                                                                     /label= N-glycos_site
Modified -site 277.270
/label= N-gros_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label- N-glycos_site
                                                                                                                                                  /label= N-glycos_site
Modified -site 161..163
                                                                                                                                                                                                                                                 Modified -site 195..197
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Modified -site 349..351
/label= N-glycos_site
Modified -site 600..602
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23-JUN-1989; US-370673.
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                                                                                                                                                                                                                                                                              /label= N-glycos_site
Modified -site 244..2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1047 BP;
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N-PSDB; Q10324.
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; 6 US-08-320-157-8.rng

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15 C;
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19..69
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                                                                                                       87 A;
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                                                                                                       1047 BP;
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 nrsgnnynngndnsnknnvnkvrngnrnynrnsndrtnnnnnnnnnnrcwandnanrnd 778
                                                                                                                                         899 nndvykvntngdaymvvsgnngrngnrhannnarmananndavssnrnrhrnh-dnnrnr 957
                                                                                                                                                                                                                                                                                                                                09-APR-1991 (first entry)
Human Natriuretic Peptide Receptor B.
NPRB; ANP; BNP; CNP; kidney failure; heart failure; protein kinase;
hyperaldosteronism; glaucoma; guanyl cyclase.
                                                                                                                                                            692 TCAGCCTCCTGTTCCTGCTGATGGTGATAAAACGTAGCTGCGGAAAACCTCCTCTGTG
                                                                                                                                                                                                      ngnnkgnnrrnnknggtsnndnnnrmnnyannnnknvnnrtnaynnnkrkanannynnn
                                                                   CATAGCGTCGGTT-GATGTCGTCCCCAATGATGGCGAGCTGCCGTCCCACCTGCCCATG
                                                                                                                  GTGCTGCTAGGTTGCAGAGGTAAGGTGACCATCTCTGGGTCGGCAGGGGCAGCCGCCCCT
                      870 CTCATAGGCATTCTCTGCCGTGGGCTGCAGGTGCTG-CAACATGGTCTGGAACTCTGAGT
                                                                                          nhsvannnkrgntvnanandsvtnynsdnvgntansanstnmnvvtnnndnytcndannd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Natriuretic protein receptor B - for diagnosis and treatment of kidney failure, heart failure, hyperaldosteronism, glaucoma etc. Claim 3; Fig 1; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and C]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "GC and protion kinase activity" Modified -site 24..26 /label= Nejlycos_site Modified -site 35..37 /label= N-glycos_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Domain
123..455
| Alabel - extracellular domain
| Anote- "binds natriuretic peptides A,B
                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                           Q10572 standard; DNA; 1047 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Omain 456..456
label= transmembrane domain
Omain 479..1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= cytoplasmic domain
/note= "GC and protien kins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-JUN-1989; US-370673.
(GETH ) GENENTECH INC.
Chang M, Goeddel D, Lowe
WPI; 91-036711/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label N-glycos_site
Modified -site 244..246
/label N-glycos_site
Modified -site 277..279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified -site 161..163
/label N-glycos_site
Modified -site 195..197
                                                                                                                                                                                                                                                                                                                                                                                                                    /label= signal sequence
Protein 12
                                                                                                                                                                                                                                     1018 nnrgdvnmkgkg 1029
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WO9100292-A.
                                                                                                                                                                                                                                                            572 GGAGGACCTGGG 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-JAN-1991.
22-JUN-1990; U03586.
23-JUN-1989; US-3706
                                                                                                                                                                                                                                                                                                                                                                                                                                             /label- mature NPBR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         351 tnnnggtrndgnrnvnkmngrryhgvtgnvvmdknndrntdnvnwamgdndsgdnnnaah 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              411 ysganknnwwtgrnnn-wvkgannsdnnncandnddnscdktnnstnanvangtgntnnm 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                364 AAAGGCTACATCCAGATGCTGGGAATGCACTGACGCCCATTCCTGGAAACTGGGCTCCCA 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         424 CICAGCCCCIGGGAGCAGCAGCCGCCAGCCCCTCGGGACCTCCATCTCCACCTGCTGAG 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           767 rcwandnanrndngnnkgnnrrnnknggtsnndnnnrmnnyannnknvnnrtnaynnn 826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 887 ndnytcndanndnndvykvntngdaymvvsgnngrngnrhannnarmananndavssnrn 946
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                827 krkanannynnnnhsvannnkrgntvnanandsvtnynsdnvgntansanstnmnvvtnn 886
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The sequence was derived from the DNA encoding natriuretic peptide receptor B, NPRB, having quanyl cyclase (GC) activity and protein kinase activity. The DNA can be inserted into expression vectors for the produ. Of the protein, opt. after being mutated to produce NPRB analogues. The protein has a mol wt. of 115 kD (calculated Mr-114,952). The protein (or variants) can be used in treatment of matriuretic peptide disorders, and also to isolate peptides using affinity chromatography. Antibodies with affinity for NPRB can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185 TTTTGGTGTATGAACTGTAGTCCTAGAGGATTTTATTAGTTATGAGTTCTATAACTAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           470 ngvssnnnnrknmnnknnasmnwrnrwnnnnngnsnryhkgagsrntnsnrgssygsnmt
|: : : : | : : : : | : : : |
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N81164;
08-NOV-1990 (first entry)
Base substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions; ss.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                        Length 1047;
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 9.3%; Pred. No. 5.42e-31;
Matches 63; Conservative 199; Mismatches 412; Indels
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Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ymrttthhyrrmrbnvyrdynrsdaaawyccyrrsvkydccynachhddhyvybbbvynv 145
                                                                                                                                                                                                                                                       WPI; 88-279927/40.
Introducing random point mutations into nucleic acods -
by prepn of single stranded template, annealing a primer, elongation, misincorporation, completion of molecules and screening.
                                                                                                                                                                                                                                                                                                                                                           Random point mutations were introduced into the alpha fragment of Erodia beta-galactosidase. The wild type sequence was obtained as a single stranded template and an oligonucleotide was hybridised to it to generate a popn of DNA molecules which terminate at all possible nucleotide positions within a specified region. The variable 3 ends generated in this way are used as primers for reverse transcriptase. Nucleotides are misincorporated by the transcriptase and the molecules are completed to forms that can be amplified and then expressed in a suitable host-vector system. The sequence covers all 176 difft base substitutions, most of which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oligonucleotide probe MKI4-A consists of nucleotides 5-95 of MKI4 (Q51735). It hybridized to all spp. of mycobacteria tested, but cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59.
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Oligonucleotide probe MK14-A
Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New oligo:nucleotide probes specific for Mycobacteria – used detection and amplification of Mycobacteria nucleic acid in
                                                                                                                                                                                               (SUSO) SUOMEN SOKERI OY.
Lehtovaara P., Knowles J., Kolvula A., Bamford J., Reinikainen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 45; DB 1; Length 204;
Pred. No. 1.24e-11;
57; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 43; DB 9; Length 91;
Pred. No. 1.70e-10;
45; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       146 hnhnncncccbnnhvchnvhbnnhrnwayvrhdarrddvhccvchcc 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           occurred singularly in any given mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47 C;
                        /function-multiple cloning site
primer_bind 187..204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LT 10
051746 standard; cDNA; 91 BP.
051746;
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01-DEC-1993.
24-MAY-1993. 108325.
26-MAY-1992; US-889651.
(BECT ) BECTON DICKINSON CO.
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Local Similarity 10.2%;
les 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 A;
                                                                                                                                                      30-MAR-1988; 105163.
03-APR-1987; US-034819.
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Sequence 204 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
Mes 12; Conser
                                                                                                      EP-285123-A.
                                                                                                                              05-MAY-1988.
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Gaps

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3 ctccggcgssvhsyyvvhvvshhhsvhhvvhhvhvvhvvhhvhhvhyhvyvsvc 61

Matches

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Introducing random point mutations into nucleic acods -

Introducing random point mutations into nucleic acods -

Thy prepr of single stranded template, annealing a primer, elongation,

misincorporation, completion of molecules and screening.

Disclosure; p; English.

Random point mutations were introduced into the alpha fragment of

E. Coll beta-galactosidase. The wild type sequence was obtained as a
single stranded template and an oligonucleotide was hybridised to

it to generate a popn of DNA molecules which terminate at all

c possible nucleotide positions within a specified region. The

variable 3' ends generated in this way are used as primers for

reverse transcriptase. Nucleotides are misincorporated by the

transcriptase and the molecules are completed to forms that can be

amplified and then expressed in a suitable host-vector system.

The sequence covers all 176 difft base substitutions, most of which
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                      New oligo:nucleotide probes specific for Mycobacteria - used for detection and amplification of Mycobacteria nucleic acid in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-NoV-1990 (first entry)
Base substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions;
Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oligonuclectide probe MK14-A consists of nucleotides 5-95 of 1051735). It hybridized to all spp. of mycobacteria tested, larges reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also 051735-45 and 051747-59.

Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SUSO) SUOMEN SOKERI OY.
Lehtovaara P, Knowles J, Koivula A, Bamford J, Reinikainen T;
WPI; 88-279927/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1204 GGGACCCCAAAGGCACCCTTGGGAGTCATGATTTGAAGAATCTTCGTACC 1155
                                                                                                                                                31-MAY-1994 (first entry)
Oligonucleotide probe MK14-A
Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.3%; Score 42; DB 9; Length 91; 0.0%; Pred. No. 6.22e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; Page 14; 23pp; English
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                                                                                                                                                                                                                                                                               01-DEC-1993.
24-MAY-1993; 108325.
26-MAY-1992; US-889551.
(BECT.) BECTON DICKINSON CO.
Shank DD, Spears PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N81164 standard; DNA; 204 BP
N81164;
                                                                                     T 11
Q51746 standard; cDNA; 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Conservative
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                                                                                                                                                                                                                                                                                                                                                                             Shank DD, Spears PA;
WPI; 93-378844/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-MAY-1988.
30-MAR-1988; 105163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain proteins bisclosure; Page 35; 255pp; Brailsh.

070468 is a generic DNA sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides This generic formula can also be represented as follows: X(NNB)11(TGC)(NNB)6Z(NNB)7(TGC)(NNB)10Y. X and Y are flanking restriction sites (X is not the same as Y) that are not specified further. Other generic sequences are shown in Q70466-68.

Other specific peptides generated by these generic sequences are shown in R55151-54. TSARs are concatenated heterofunctional proteins or peptides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                have designed activity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The TSARS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        target or on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                comprising at least two functional regions - a binding domain with affinity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker peptide between the 2 domains. The oligonucleotides are also designed so that the expressed peptide contains 2 or 4 cysteine residues positioned in, or flanking, the unpredicted or variant residues. These residues confer some degree of conformational rigidity to the peptides. The TSARS or compans, comprising a TSAR binding domain can be used in vivo to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     deliver a chemically or biologically active molety, eg. metallion, radioisotope, peptide, toxin or enzyme, to the specific target or on teal. They can also replace the function of macromolecules, eg. monoclonal or polyclonal antibodies and therefore circumvent the need
                                                                                                                                             281 AACATCATTTAAAAAACATTTTTGGCTGGCACCTCATGATCACTGGAGTCTCGCGGGTC 340
                                                                                                                   95 rrmrbnvyrdynrsdaaawyccyrrsvkydccynachhddhyvybbbvynvhnhnncncc 154
                                                                                                                                                                                                                                                                                                            Generic DNA sequence to generate a random TSAR petide library. TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concatenated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
                                                                                         Gaps
                                  108 Others;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designe allowing direct and rapid detection in a screening process. Sequence 114 Bp. 0 A; 2 C; 2 G; 2 T;
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Pred. No. 1.26e-06;
34; Mismatches 74; Indels
                                                           Length 204;
                                                                                         34; Indels
                                 11 T;
                                                                                                                                                                           155 cbnnhvchnvhbnnhrnwayvrhdarrddvhccvchccgat 195
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                                                                          Pred. No. 8.16e-09
                                                            DB 1;
                                                                                         53; Mismatches
                               17 G;
occurred singularly in any given mutant. See also P80575. Sequence 204 BP; 21 A; 47 C; 17
                                                            Score 40;
                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers 55..60
                                                                                                                                                                                                                                                                Q70468 standard; DNA; 114 BP.
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Fowlkes DM, Ray BK;
WPI; 94-279739/34.
                                                                          12.9%;
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                                                                                        Conservative
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US-176500.
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/note= "this sequence
--- of 6, 9 or 12
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01-FEB-1994; U00977
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Matches 4; Conser
                                                                        Best Local Similarity
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30-DEC-1993;
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Gaps

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Similarity 3.6%; 4; Conservative

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screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain proteins comprising a binding domain and an effector domain broteins of 2016 of 20 separate page 35, 25pp; English.

O70466 is a generic DNA sequence used to generate random TSAR (Totally Synthetic Affainty Reagents) peptides. This generic formula can also be represented as follows:X(NNB)1(TGC)(NNB)10(TGC)2(NNB)4X(NNB)8(TGC)(NNB) (TGC)2(NNB) (TGC)2 (NNB) (TGC)2 (TNB) (TG
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                                                                                            909 CATCAAITGGGGCCGTGTGGTGGCTCTTCTGGGCTTCAGCTACCGTCTGGCCCTACACAT 968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Generic DNA sequence to generate a random TSAR-9 petide library. TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
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bոռbոռbոռbոռbոռbոռbոռbոռbոռbոռbեցcոռbոռbոռbոռbոռbոռbոռbոռbոռnnո 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 nbanbanbanbanbanbanbtgcanbanbanbanbanbanbanbanb 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence represents 'Z'; Z can be a 5, 9 or 12 nucleotides (see
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Pred. No. 1.26e-06;
31; Mismatches 71
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Q70466 standard; DNA; 114
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D2 0701657

D3 0701657 Standard, DNA; 114 BP.

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993 CCTGGGCCAGGTGACCCGCTTTGTGGTGGACTTCATGCTGCATCACTGCATT 1044

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                                                                   Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, Distribution rights by IntelliGenetics, Inc.
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123:EST123
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168:EST168
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167:EST167 1
172:EST172 1
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157:EST157
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(1-1287) from US08320157.seq
1287
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AAAATTATATTTAATTACAC.
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106:EST106
116:EST116
1116:EST116
1116:EST116
113:EST112
113:EST112
114:EST14
114:EST14
114:EST14
115:EST15
116:EST16
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116:EST16
116:EST16
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Listing first 45
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Perfect Score:
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Run

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H. saplens partial co 4.59e-05 and 22121.11.11 Homo saple 4.59e-05 y13707.11 Homo saple 4.59e-05 y13707.11 Homo saple 4.59e-05 z20110.11 Homo saple 4.59e-05 z20110.11 Homo saple 4.59e-05 x98f11.13 Homo saple 4.59e-05 y95404.11 Homo saple 4.59e-05 x96609.11 Homo saple 4.59e-05 x96609.11 Homo saple 4.59e-05 z201800.11 Soares fet 4.59e-05 x201900.11 Soares fet 4.59e-06 yqq5009.11 Homo saple 7.34e-04 yqq5009.11 Homo saple 7.34e-04 yqb8000.11 Soares mou 7.34e-04 ybb8000.11 Soares mou 7.34e-04 ybb3000.11 Homo saple 7.34e-04 z201008.11 Homo saple 7.34e-04 z201008.11 Homo saple 7.34e-04 z201008.11 Homo saple 7.34e-04 z201002.11 Homo saple 7.34e-04 z201001.11 Soares fet 7.34e-04 z401000.11 Soares fet 7.34e-04 z40
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0.00e+00
4.27e-87
4.27e-87
3.44e-64
7.53e-39
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   179:EST179
184:EST184
189:EST189
194:EST194
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176:EST176 177:EST177 178:EST178 181:EST181 182:EST182 183:EST183 186:EST186 187:EST187 198:EST188 191:EST191 192:EST197 198:EST193 196:EST196 197:EST197 198:EST198
                                                                                                                                                                                                                                                                          Description
                                                                                                              scale
                                                                                                          Variance 2.183;
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W34930
W34930
W41038
AA101808
HUM403H04B
AA001756
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WA42014
WA42014
AA050569
M83998
W82028
AA139013
H3C07H082
HSC3LC012
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HUM229F11B
HUM250H12B
HSCOME041
AA138853
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R67853
HSC2SG051
AA169681
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T54824
AA173916
N72841
W17230
AA0365
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 175:EST175
180:EST180
185:EST185
190:EST190
195:EST195
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embryo NbME13.5 14.5 Mus musculus CDNA to SW:BCLX\_HUMAN Q07817 APOPTOSIS REGULATOR

A016399 497 bp mi mg88g02.rl Soares mouse en clone 440114 5' similar to BCL-X.;. AA016399 g1478767

DEFINITION

ACCESSION NID

02-AUG-1996

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Query Match
Best Local Similarity 95.7%;
Matches 291; Conservative
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BASE COUNT
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AUTHORS
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JOURNAL
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1 (bases I to 497)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,

Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,

Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,

Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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                                         Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
                                                                                                                                                                                                             Contact: Marra M/Mouse EST Project
Washl-HHMI Mouse EST Project
Washlordon University School of MedicineP
Washlordon University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1229 TTAAGTCCAGGCAGGGGTCTGAACTGGGACCCCAAAGGCACCCTTGGGAGTCATGATTTG 1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ctggcgatgtaatgatgcagtatgatatcagccaaaaagcaggtcacctggcccaggaag 261
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Pred. No. 0.00e+00;
0; Mismatches 101; Indels 0;
                                                                                                                                                                                                                                                                                                                                                          Possible reversed clone: similarity on wrong strand Seq primer: -28M13 rev2 from Amersham High quality sequence stop: 484.
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4
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                                                                                                                                                         Waterston, R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="embryo"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 78.7%;
Matches 374; Conservative
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             house mouse.
Mus musculus
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JOURNAL
COMMENT
KEYWORDS
SOURCE
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                                                                                                   AUTHORS
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Eukaryotae: Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archorta; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 303)
11 (bases 1 to 303)
11 (bases 1, Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Hersston, R., Williamson, A., Wohldmann, P. and
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Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              322 accacgcggccccagctgatgccactcttaaataggctggaggcgatcttggtgaagagt 381
                                                                                                          382 tcgtaggcattcccggctgtgggctgaagctgttctagtaaattctggaactctgtgtcg 441
coggicaaaccacgciggiagacgiacagggccagacggiagccaaagcccaggagaggcc 321
                      869 TCATAGGCATTCTCTGCCGTGGGCTGCAGGTGCTGCAACATGGTCTGGAACTCTGAGTCA
                                                                                                                                                                                                                                                 Contact: Wilson RK
WashU-Merck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 303;
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/organism="Homo sapiens"
/clone="231262"
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AUTHORS
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Bacsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoc,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                'n
                                                                                                                                                                                                                                                                 545 bp mRNA EST 11-SEP-1996
Soares mouse p3NMF19.5 Mus musculus cDNA clone 329622
SW:BCLX_HUMAN Q07817 APOPTOSIS REGULATOR BCL-X.;
                                                                                                                                                                                                                                                                                                                                                                Eukaryotae, mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington University School of MedicineP
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                           672
                                                cagcaggaacaggaggctgaaggggcggctgctgacnc-gacccagagatggtcacctta 179
gaggagcaggtagcccaggacacagaggaggttttccgcagctacgtttttaccaccat
                                                          MGI:211022
Possible reversed clone: similarity on wrong strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism-"Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 411.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   primer: ETPrimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                         Mus musculus
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mb16g04.rl S
similar to S
W42014
                                                                                                                                                                                                                                                                                                                                           house mouse.
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JOURNAL
COMMENT
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AUTHORS
61
                                                                                                                                                                                                                                                                                                      ACCESSION
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KEYWORDS
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AA049970 446 bp mRNA EST 09-SEP-1996 mj39b01.rl Soares mouse embryo NDME13.5 14.5 Mus musculus cDNA clone 478441 5' similar to SW:BCLX_HUMAN Q07817 APOPTOSIS REGULATOR
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                           1109 AGGATGGGACCATTGCCCAAGTTCAGGGCTGCCACCCAGCCACCCCTCTGTGCAATCCAC 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         149 aggatggggactctacgaaaattcagggctgccacccaaccgcctctgtgcgatccat 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ctggcgatgtaatgatgcagtatgatatcagccaaaaagcaggtcacctggcccaggaag 268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         989 CCAGTCAGGCCACGCTGGTAGATGTGTAGGGCCAGACGGTAGCTGAAGCCCAGAAGAGCC 930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   accacgcggccccagctgatgccactcttaaataggctggaggcgatcttggtgaagagt 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     929 ACCACACGCCCCAATTGATGCCACTCTCAAACAGGCTGGAGGCAATCTTGGTGAAGTAC 870
                                                                                                                                                                                                                                                      88
                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                   31 tttagtccagccaggcacgtgg-ctggggccccagtgggtcccc-gggagtcatgatctg
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
                                                                                                                                                                                               Š.
                                                                                                                                        Length 545;
                                                            others
                                                                                                                                                                                            Indels
/lab_host="DH10B (ampicillin resistant)"
<1...>545
1 139 c 165 g 105 t 2 other
                                                                                                                                                                                               Mismatches 100;
                                                                                                                                        Score 254; DB 153;
Pred. No. 0.00e+00;
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source

FEATURES

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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Gelsel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                           Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                        Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     187 cgatgagtc--ccc-gtcc-c--cttctgaacagcaggtgcccaggacacagaggaggt 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCUS AA050569 361 bp mRNA EST 09-SEP-1996 DEFINITION mj16b12.rl Soares mouse embryo NbME13.5 14.5 Mus musculus CDNA clone 476255 5'.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Marra M/Mouse EST Project
WashD-HHMI Mouse EST Project
WashIngton University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Soares mouse embryo NbME13.5 14.5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Watch 5.6%; Score 72; DB 138; Length 292; Local Similarity 79.7%; Pred. No. 4.27e-87; Les 137; Conservative 0; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: -28M13 rev2 from Amersham
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
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The WashU-HHMI Mouse EST Project
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88
                                                                                                                                                                                                                                       Unpublished (1996)
                                              Mus musculus
                          house mouse
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                                                                                                             REFERENCE
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Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This Clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:289185
Possible reversed clone: similarity on wrong strand
Seg primer: -28M13 rev2 from Amersham
High quality sequence stop: 319.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1180 GTCATGATTTGAAGAATCTTCGTACCACAAACTGGCCCAACAGAACCACCACCAGAACCA 1121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mj09a09.rl Soares mouse embryo NbMEl3.5 14.5 Mus musculus CDNA AA049828
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1000 GGCCCAGGAAGCCAGTCAGGCCACGCTGGTAGATGTGTAGGGCCAGACGGTAGCTGAAGC 941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              311 ccaggagagagccaccacgcgggccccagctgatgccactcttaaataggctggaggcgatct 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   371 tggtgaagagttcgtaggcatttccggctgtgggctgaagctgttctagtaaattcttga 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Soares mouse embryo NDME13.5 14.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 232; DB 138; Length 44
Pred. No. 0.00e+00;
0; Mismatches 72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
<1.5446
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                                                                                                                                                                             /organism-"Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="unknown'
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Best Local Similarity 80.9%;
Matches 304; Conservative
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BASE COUNT ORIGIN

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RESULT

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heart, Lambda ZAP Express vector-Lambda ZAP Express host-E. coll XL1-Blue Raitel-Ecorl Rsite2-Xhol mRNA was purified from human fetal hearts (8-10 weeks). CDNA was synthesized using a Xhol-Oligo diaptor-primer. Ecorl adaptors were ligated, followed by digestion with Xhol, for directional cloning into predigested lambda ZAP Express.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 270)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
   KK4271F\ \mbox{Homo} sapiens cDNA clone KK4271\ \mbox{S}' similar to BAK FOR BCL-2 HOMOLOGUE.
                                                                                                                                                                                                                                         Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygil; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 232)
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human clone=KK4271 primer=GAAATTAACCCTCACTAAAGGG library=Fetal
                                                                                                                                                                                                                                                                                                                                                                                                                          Molecular Cardiology
University of Toronto
Banting Institute, 100 College St., Toronto, Ontario, M5G1L5
Tel: 4169788758
Exa: 4169785650
Email: liewcc@utcc.utoronto.ca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 232;
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Pred. No. 3.44e-64;
0; Mismatches 2; Indels
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WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
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<1..>232
                                                                                                                                                                                                                                                                                                                                                   cDNAs from fetal heart
Unpublished (1996)
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4.7%;
Best Local Similarity 96.9%;
Matches 62; Conservative
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                                                                                                                                                                                                                        Homo sapiens
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LOCUS
DEFINITION
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JOURNAL
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptce,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                          Contact: Marra M/Mouse EST Project
WashU-HMIM Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
HMAGE Consortium (info@image.llnl.gov) for further information.
MG1:286999
                                                                                     Eukaryotae, mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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/sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            310 ctttcgaagctacgttttttacctccaccagcaggaacaggagacccagggg 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 72; DB 139; Length 361;
Pred. No. 4.27e-87;
0; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: -28M13 rev2 from Amersham.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
                                                                                                                                                                                                                                     Waterston, R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 5.6%;
Best Local Similarity 79.7%;
Matches 137; Conservative
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                                                                        Mus musculus
                                                     house mouse.
AA050569
91530241
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/organism="Rattus sp."
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Fax: 3018699423
                                                                                       MGI:361866
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a
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Galsel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Thetsing, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                    This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:247664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA139013 320 bp mRNA EST 02-DEC-1996 mr04a06.rl Soares mouse 3NbMS Mus musculus cDNA clone 596434 5' AA139013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vartebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  201 ctgcgatgagtccccgtcc-c--cttctgaacagcaggttgcccaggacacagaggt 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143 ctccaccaagacctgaaaaatggcatctggacaaggaccaggtcccccgaaggtgg-gt- 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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WashU-HMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 46; DB 175; Length 270; Pred. No. 7.53e-39;
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                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="19.5 dpc total fetus"
/lab_host="DH108 (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Soares mouse p3NMF19.5"
                                                                                                                                     Seq primer: -28M13 rev2 from Amersham.
Location/Qualifiers
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                                                                                                                                                                                       /organism-"Mus musculus"
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The WashU-HHMI Mouse EST Project
                                                                      mouseest@watson.wustl.edu
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3.6%;
Bost Local Similarity 76.7%;
Matches 102; Conservative
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JOURNAL
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rat primer=M13 Reverse library=Rat PC-12 cells, untreated vector=pBluescript SK- Rsitel=EcoRI Rsite2=XhoI poly(A)+ RNA was purified from untreated PC12 cells cultured for 9 days. cDNA was constructed using an oligo-dr primer and directionally cloned using the Lambda ZAP II Vector Kit by Stratagene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Rattus.

1 (Joses 1 to 279)
Lee, N.H., Weinstock, K.G., Kirkness, E.F., Earle-Hughes, J.A., Fuldner, R.A., Marmaras, S., Glodek, A., Gocayne, J.D., Adams, M.D., Comparative expressed sequence tag analysis of differential gene expression profiles in PC-12 cells before and after nerve growth factor treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-SEP-1995
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For clone availability please contact the TIGR Database (tdbinfoetdb.tigr.org).
Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     264 cogtoccottotgaacagoaggttgcccaggacacagaggaggtctttcgaagctac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    601 CCCTCTGCTTCTGAGGAGGAGGTAGCCCAGGACACAGAGGAGGTTTTCCGCAGCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. USA 92, 8303-8307 (1995)
Other_ESTs: EST106322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 39; DB 186; L
Pred. No. 5.11e-27;
0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Lee NH
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
                                                                                                 Seq primer: -28M13 rev2 from Amersham
                                                                                                                                                                     /organism-"Mus musculus"
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/lab_host="DH10B"
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                                                                                                                    Location/Qualifiers
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84.2%;
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C
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Matches 48; Conservative
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (19-JAN-1995) Genethon, B.P. 60, 91002 Evry Cedex France and Genetique Moleculaire et Biologie du developpement, CNRS UPR420 B.P. 8, 94801 Villejuif Cedex France.E-mail: genexpress@genethon.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cloning_method: total mRNA was oligo-(dT) primed and directionally cloned 5' -> 3' into the HindIII -> NotI sites of the lafmid BA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Mases 1 to 266)

(Mases 1 to 266)

(Mases 1 to 266)

Devignes, C., Behar, G., Bois, F., Bouchier, C., da Silva, C.,

Devignes, M.D., Duprat, S., Houlgatte, R., Jumeau, M.N., Lamy, B.,

Lorenzo, F., Mitchell, H., Mariage-Samson, R., Pietu, G., Pouliot, Y.,

Sebastian-Kabaktchis, C. and Tessier, A.

IMAGE: molecular integration of the analysis of the human genome
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                                                                                                                                                                                                                                                                   21-SEP-1995
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                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases i to 266)
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                                                                                                                                                     277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA sequence complementary to mRNA (3'end)
Stretch_removed: removed at sequence 5'end
Normalization_method: Bento Soares, P.N.A.S in press;
Genexpress_library_idt: C;
Genexpress_sequence_idt: al--07h08.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                      9645167
partial cDNA sequence; transcribed sequence fragment.
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                                                                            Length 279;
                                                                                                                                                   226 cctccaccaagaccggaaaaatggcatccgggacaaggaccaggtnctncca
                       5 others
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                                                                                                                                                                                                                                                   HSC07H082 266 bp RNA EST
H. sapiens partial cDNA sequence; clone c-07h08.
F01610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing_method: single read, full automatic;
Primer: (-21)M13_universal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    161 aataaaaatttaaatatttttgaactgaataataataaa 200
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Pred. No. 4.59e-05;
0; Mismatches 8
                                                                                              1.48e-14;
                                                                        DB 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="total brain"
/dev_stage="3 months old"
47 c 49 g 75 t
                                                                                                               0; Mismatches
                     53
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                                                                          Score 31;
Pred. No.
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Unpublished
                   16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="female"
                                                                        2.4%;
larity 82.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 1.9%;
Best Local Similarity 80.0%;
Matches 32; Conservative
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 <1..>279
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                                                                                            Local Similarity
les 43; Conser
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                                                                          Query Match
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55 AATAAAATTCAAATGTTATAGAACTGAAAAAGATGAAAA 94

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Direct Submission
Submitted (19-JAN-1995) Genethon, B.P. 60, 91002 Evry Cedex France
and Genetique Moleculaire et Biologie du developpement, CNRS UPR420
B.P. 8, 94801 Villejuif Cedex France. E-mail:
genexpress@genethon.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cloning_method: total mRNA was oligo-(dT) primed and directionally cloned 5' -> 3' into the HindIII -> NotI sites of the lafmid BA
                                                                                                                                                                                                                                                                                                                                                                                                The Genexpress cDNA program
Unpublished

(base)

Auffazy,C., Behar,G., Bois,F., Bouchier,C., da Silva,C.,

Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B.,

Corenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y.,

Sebastiani Rabaktchis,C. and Tessier,A.

IMAGE: molecular integration of the analysis of the human genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stretch_removed: removed at sequence 5'end
Normalization_method: Bento Soares, P.N.A.S. 91:9228-9232(1994);
Genexpress_library_idt: C;
Genexpress_sequence_idt: alc-31c01.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /isolate="muscular atrophy patient" /clone_lib="normalized infant brain cDNA from B.Soares,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N92UlU 358 bp mRNA EST 04-APR-1996 2a2la11.r1 Homo saplens cDNA clone 293180 5' similar to gb:M10942_cds1 Human metallothlonein-Ie gene (HUMAN);. N92010 91264319
                 21-SEP-1995
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                                                                                                                                                             Eukaryotee; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; H
1 (bases 1 to 337)
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                                                                                                 partial cDNA sequence; transcribed sequence fragment
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HSC3LC012 337 bp RNA EST
H. sapiens partial cDNA sequence; clone c-3lc01.
F10881
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CDNA sequence complementary to mRNA (3'end)
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Pred. No. 4.59e-05;
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/dev_stage="3 months old"
78 c 92 g 64 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 1.9%;
Best Local Similarity 69.4%;
Matches 43; Conservative
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                                                                                                                                              Homo sapiens
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Wilson, R.
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Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichtys;
Sarcopterygil; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archorta; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 395)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
                                                                                                                                                                                                                                                                                                                                                                            Deuterrogical, macros, contractions, continued, better the state of th
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Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Location/Qualifiers
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WashU-Merck EST Project
Washington University School of Medicine
4444 Porest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
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Pred. No. 4.59e-05;
0; Mismatches 11; Indels
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Yj3707.rl Homo sapiens cDNA clone 150924 5'
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Matches 34; Conservative
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/note="Organ: heart; Vector: pT/T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCOTSCAGCGGCCGCACATCTTTTTTTTTTTTTTTTTT] double-stranded cDNA was size selected, ligated to Eco RI
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444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Feb. 314 286 1810
Email: est@watson.wustl.edu
Email: est@watson.wustl.edu
IMAGE Cone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1099 std Error: 0.00
Seq primer: mob.REGA-ET.
                                                                                                                                                                                                                                                                                                                                                                                          High qulity sequence stops: 314
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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2491f166.81 Soares fetal heart NbHH19W Homo sapiens cDNA clone
W84628
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Bukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;

Vertebrata; Eutheria; Primates; Catarrhin; Hominidae; Homo.

(Dassa; Lo 409)

Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holfman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,

Parsons,J., Rikful,L., Rohlfing,T., Soares,M., Tan,F.,

Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
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                                                                                  Wilson, R.
The WashU-Merck EST Project
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Best Local Similarity 80.08;
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                                                                                                                                            Unpublished (1995)
                                                                                                                                                                                                    Contact: Wilson RK
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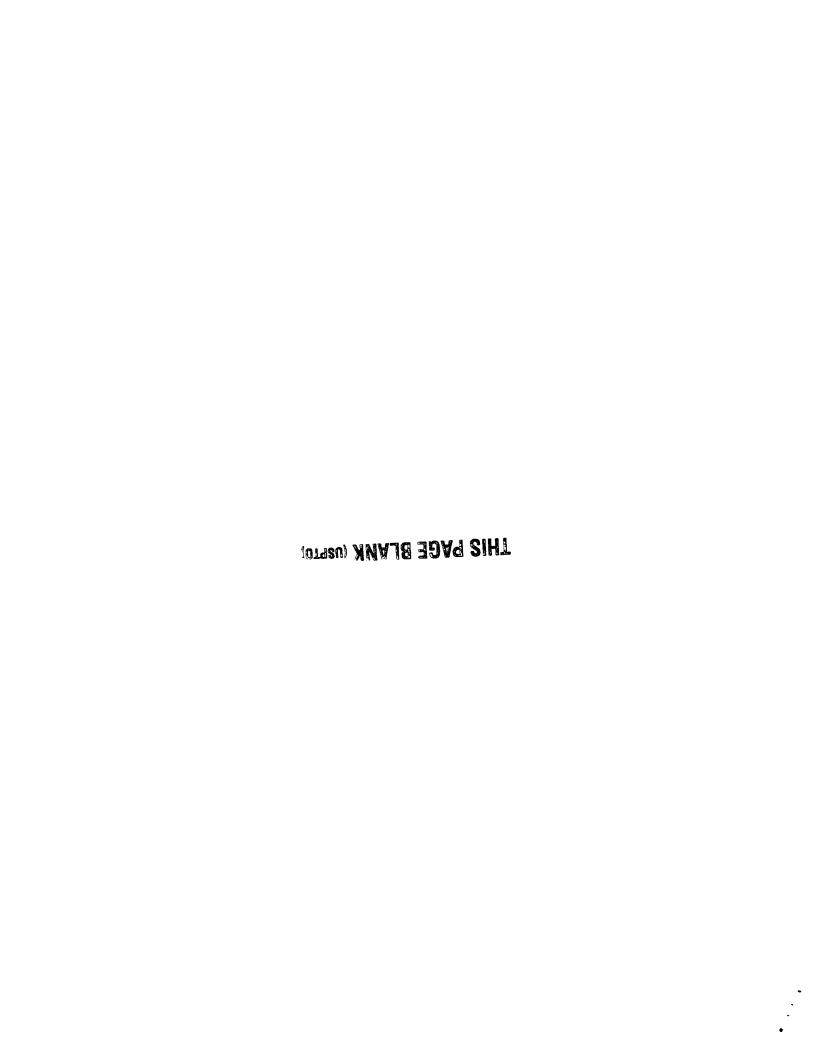
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adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT713 vector (Pharmacia). Library went through one round of normalization to a CCL = 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NBHL19w."

/clone_11b="Soares fetal heart NBHH19w"
//dev_stage="19 weeks"
//dev_stage="19 w
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Search completed: Thu Aug 21 13:59:38 1997 Job time: 2124 secs.

326 ct 327 || 589 CT 588

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5.87e-129 2.88e-54 2.88e-54 2.02e-28 2.02e-28 2.02e-28 8.38e-27

G06794 MM1142620 AA185611 AA185611 AA123834 AA123834 AA139013 AA139013 AA139013 AA139013 AA184020 AA184020 AA184020 N98063

human STS WI-7983

Description

В

Length

Match

Score

No.

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	(MI)
Release 2 Copyright Di	e 2.1D John F. Collins, Biocomputing Research Unit. jht (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by Intelligenetics, Inc.
MPsrch_nn n.a.	- n.a. database search, using Smith-Waterman algorithm
Run on: Tabular output no	Thu Aug 21 14:00:02 1997; MasPar time 343.89 Seconds 1028.472 Million cell updates/sec not generated.
itle: escript	>US-08-320-157-8 (1-1287) from US08320157.seq
Perfect Score: N.A. Sequence: Comp:	1287 1 TITTAATATAAATTAATGGCCTCAAGAGTACAGAAGCTT 1287 AAAATTATATTAATTACACGGAGTTCTCATGTCTTGGAA
Scoring table:	TABLE default Gap 6
Nmatch STD:	Dbase 0; Query 0
Searched:	359085 segs, 137405154 bases x 2
Post-processing:	Minimum Match 0% Listing first 45 summaries
Database:	EST-STS-THREE  1:EST199 2:EST200 3:EST201 4:EST202 5:EST203 6:EST204  7:EST205 8:EST210 14:EST201 11:EST209 11:EST210  13:EST211 14:EST212 15:EST213 15:EST214 17:EST215  18:EST211 14:EST212 25:EST213 16:EST214 17:EST215  23:EST212 14:EST22 25:EST223 26:EST224 27:EST225  23:EST223 34:EST223 25:EST223 26:EST224 27:EST225  23:EST23 34:EST23 23:EST223 36:EST229 32:EST230  33:EST23 14:EST32 35:EST233 36:EST23 32:EST230  46:EST21 47:EST32 35:EST233 36:EST23 32:EST230  46:EST31 47:EST32 48:EST33 36:EST3 37:EST23 45:EST30  46:EST31 47:EST32 48:EST3 56:EST3 36:EST36 44:EST5 64:EST37 43:EST3 57:EST36 45:EST36  49:GNEST1 50:GNEST2 51:GNEST3 52:GNEST4 63:GNEST15 64:GNEST1 66:GNEST1 66:GNEST1 66:GNEST1 67:GNEST2 77:GNEST2 77:GNES
Statistics:	_

8.38e-27 1.07e-07 1.07e-07 3.38e-05 3.33e-05 3.33e-05 3.33e-05 3.33e-05 3.33e-05 3.33e-05 5.10e-04 6.10e-04 6.10e-04

N97744 AA138853 MMAA89753

AA198152 N59408 AA126907

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AA115608 AA115608 AA115474 N58693 G14786

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G06794 1258 bp DNA STS 19-OCT-1995
CON human STS WI-7983.
DN G06794
G06039
STS sequence; primer; sequence tagged site.
human STSs derived from sequences in dbEST and the Unigene
collection.
SM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Gnathostomatta; Ostelchthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutherla; Archonta; Primates;
Catarrhini; Hominidae; Homo. Genome Research; Physically Contact: Thomas Hudson Whitehead Institute/MIT Center for Genome Research Whitehead Institute for Biomedical Research forCenter 1 (bases 1 to 1258) Hudson,T. Whitehead Institute/MIT Mapped ESTs Unpublished (1995) LOCUS DEFINITION ORGANISM REFERENCE AUTHORS TITLE ACCESSION NID JOURNAL COMMENT KEYWORDS SOURCE RESULT

Stratagene Soares NhH (

zq10f12.rl st zr77f05.rl so mt62e08.rl S

ALIGNMENTS

AA121520 AA182287 BM4163 AA197101 AA250729 MMAA85558

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Human brain cDNA (fet zol2h07.sl Stratagene human STS SHGC-10121. mz84f08.rl Soares mou mz84f08.rl Soares mou m718670.zapprdd2.l, Dhuman STS WI-11990. CpEST.117 pSKIIminusC cpEST.117 pSKIIminusC zk88910.sl Soares pre mt76h12.rl Soares mou RRAWGA12755K Brugia m

HUMSUPY306
AA130593
G14445
AA254866
AA254866
N97957
G21837
CAA24645
CPAA24645

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MMAA31246

AA189753 AA231246

No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, derived by analysis of the total score distribution. score gand is Pred.

SUMMARIES

Result

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281..625
/map="751_A_7; 787_E_4; 908_C_6; 923_D_2; 919_D_10; 942_A_12; 808_G_6,11]"
281..300
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complement(606..625)
/map="751_A_7; 787_E_4; 908_C_6; 923_D_2; 919_D_10; 942_A_12; 808_G_6,11)"
6 a 356 c 355 g 301 t 10 others
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21-FEB-1997 (Rel. 51, Created)
22-FEB-1997 (Rel. 51, Last updated, Version 2)
mt62e08.rl Soares 2NMT Mus musculus cDNA clone 634454 5' similar
to TR:G595926 G595926 BAK-2 PROTEIN.;
                                                                                                                                                                                                                                                                                                  Prepared with primer pairs derived from U16811 -- Unigene.
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1258;
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9 Cambridge Center, Cambridge MA 02142 USA
Tel: 617 252 1900
Fax: 617 252 1902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 94; DB 38; L
Pred. No. 5.87e-129;
0; Mismatches 4;
                                                                                                                                                                                                       0.025 units/ul
                               Email: thudson@genome.wi.mit.edu
                                                                                                       Denaturation:
Annealing: 56 degrees C
Polymerization:
PCR Cycles: 35
Thermal Cycler:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LT 2
MM1142620 standard; RNA; EST; 133 BP.
AA185611;
                                                   Primer A: CTGATAACTTGGGGGGGAA
Primer B: GAGAGTCCAACTGCAAAGGC
STS size: 345
PCR Profile:
                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1..1258
                                                                                                                                                           Protocol:
Template: 10 ng
Primer: each 5 pM
dNTPs: each 4 nM
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                                                                                                                                                                                                                                            MgC12: 1.5 mM
KC1: 50 mM
Tris-HCL: 10 mM
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Total Vol: 20 ul
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Best Local Similarity 95.4%;
Matches 104; Conservative
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                by Dr. Bertrand Jordan. Library went through two round normalization, and was constructedby Bento Soares and M.Fatima Bonaldo."
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                                                                                                                                                                             Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, Mo 63108 Tel: 314 286 1800 Fast: 314 286 1810 Email: mouseest@watson.wusll.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:386446 Trace considered overall poor quality Possible reversed clone: similarity sequence stop: 1.
Dubuque T., Geisel S., Kucaba T., Lacy M., Le M., Martin J., Morris M., Schellenberg K., Steptoe M., Tan F., Underwood K., Moore B., Theising B., Wylle T., Lennon G., Soares B., Wilson Materston R., The Washu-HHMI Mouse EST Project";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Soares 2NbMT" /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism-"Mus musculus"
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The WashU-HHMI Mouse EST Project
Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH108"
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Mus musculus
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Stepto,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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                                                                                                                                                                                                                                                       This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Possible reversed clone: similarity on wrong strand
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 1.
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                                     Contact: Marra M/Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
                                                                                                                                                                                                                     Email: mouseest@watson.wustl.edu
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/lab_host="DH10B"
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Best Local Similarity 81.6%;
Matches 71; Conservative
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Thelsing,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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mp93c04.r1 Soares 2NbMT Mus musculus cDNA clone 576774 5' similar
to TR:G595926 G595926 BAK-2 PROTEIN. ;.
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Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
WashIngton Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: mousest@watson.wustl.edu
This clone is available royalty.free through LLNL; contact the
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Possible reversed clone: similarity on wrong strand
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 1.
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Washington University School of MedicineP
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/clone_lib="Soares 2NbMT"
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The WashU-HHMI Mouse EST Project
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                                Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:351422
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25-MOV-1996 (Rel. 50, Created)
19-FEB-1997 (Rel. 51, Last updated, Version 2)
mp93c04.rl Scares 2NDMT Mus musculus cDNA clone 576774 5' similar
to TR:G595926 G595926 BAX-2 PROTEIN. ;
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Forest Park Parkway, Box 8501, St. Louis, MO 63108
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Pred. No. 2.02e-28;
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Location/Qualifiers
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Best Local Similarity 78.2%;
Matches 104; Conservative
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and Eco RI sites of the modified pT7T3 vector. RNA provide
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Gesel, S., Kucaba, T., Lacy, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
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mp3c04.r1 Soares 2NbMT Mus musculus cDNA clone 576774 5' similar
AA123834
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                            Seq
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royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:351422 primer: -28M13 rev2 from Amersham.
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Sequence 310 BP; 72 A; 96 C; 86 G; 55 T; 1 other;
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0; Mismatches 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 98;
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/clone_lib="Soares 2NbMT"
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                                                                                                                                              /organism="Mus musculus"
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The WashU-HHMI Mouse EST Project
Unpublished (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="Thymus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="4 weeks"
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                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host-"DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 3.1%;
Best Local Similarity 78.2%;
Matches 104; Conservative
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Galsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAZZO617 331 bp mRNA EST 10-FEB-1997
my25f11.rl Barstead mouse pooled organs MPLRB4 Mus musculus CDNA
clone 696909 5'.
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     This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:361866 Seg primer: -28M13 rev2 from Amersham.
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 320;
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Pred. No. 8.38e-27;
0; Mismatches 9;
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/sex="male"
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                                                                                                            /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="Spleen"
/dev_stage="4 weeks"
/lab_host="DH108"
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84.2%;
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                                                                                                 1 (bases 1 to 320)
Marra,M. Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
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This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:351422
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
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Pred. No. 2.02e-28;
0; Mismatches 22; Indels
                                                    Seq primer: -28M13 rev2 from Amersham.
Location/Qualifiers
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The WashU-HHMI Mouse EST Project
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/dev_stage="4 weeks"
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Matches 104; Conservative
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Marra M., Hillier L., Allen M., Bowles M., Dietrich N.,
Dubuque T., Gelsel S., Kucaba T., Lacy M., Le M., Martin J.,
Morris M., Schellenberg K., Steptce M., Tan F., Underwood K.,
Moore B., Theising B., Wylie T., Lennon G., Soares B., Wilson R.,
Waterston R.;
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13-FEB-1997 (Rel. 50, Created)
13-FEB-1997 (Rel. 50, Last updated, Version 1)
my25f11.r1 Barstead mouse pooled organs MPLRB4 Mus musculus cDNA
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Vartebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Pred. No. 8.38e-27;
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/lab_host="DH10B"
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Matches 48; Conservative
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by Dr. Bertrand Jordan. Library went through three rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Dubuque T., Geisel S., Kucaba T., Lacy M., Le M., Martin J.,
Morris M., Schellenberg K., Steptoe M., Tan F., Underwood K.,
Moore B., Theising B., Wylie T., Lennon G., Soares B., Wilson
Waterston R.;
"The WashU-HHMI Mouse EST Project";
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                                                                                                                                                                                                                                                                                                                                                            19-FEB-1997 (Rel. 51, Created)
19-FEB-1997 (Rel. 51, Last updated, Version 1)
mt22d08.rl Soares mouse 3NbMS Mus musculus cDNA clone 621807
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                                                                        Length 331;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP; 150 A; 56 C; 67 G; 202 T; 0 other;
mRNA <1..>331
Sequence 331 BP; 78 A; 104 C; 89 G; 60 T; 0 other;
                                                               Score 39; DB 108; I
Pred. No. 8.38e-27;
0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Soares mouse 3NbMS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
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/dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                               standard; RNA; EST; 475
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llarity 76.0%;
Conservative
                                                                   3.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (house mouse)
                                                                                                                  48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <1..>475
                                                                 Query Match
Best Local Similarity
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DEFINITION ACCESSION NID

7,7

SOURCE

KEYWORDS

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

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l (bases 1 to 228)
Dame, J.B., Arnot, D.E., Bourke, P., Chakrabarti, D., Christodoulou, Z., Coppel, R., Comman, A., Craig, A., Fischer, K., Foster, J., Goodman, N., Hinterberg, K., Holder, A.A., Holt, D., Kemp, D., Lanzer, M., Lim, A., Newbold, C., Ravetch, J.V., Reddy, G. R., Rubio, J., Schuster, S. M., Su, X.-Z., Thompson, J.K., Vital, F., Wellems, T.E. and Werner, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N98063 228 bp mRNA EST 18-NOV-1996 2149G3 czapPFDd2.1, Debopam Chakrabarti Plasmodium falciparum CDNA
                                                                                                                                                                                                                                                                                                                                                                              This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryotae; mitochondrial eukaryotes; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                             Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 26; DB 13; Length 475; Pred. No. 1.07e-07; 0; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            MGIT 1382631
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 438.

Tocation/Qualifiers

Coe //organism="Masulus" / Strain="CS7BL/6J" / Strain="CS7BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Soares mouse 3NbMS"
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Best Local Similarity 76.0%;
Matches 38; Conservative
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 Mus musculus
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AUTHORS
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., La,M., Martin,J., Morris,M., Schellenberg,K., Steptce,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:882631
                               AA184020 475 bp mRNA EST 17-FEB-1997 mt22d08.rl Soares mouse 3NbMS Mus musculus cDNA clone 621807 5' AA184020
                                                                                                                                                              Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                            Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Pred. No. 1.07e-07;
0; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seg primer: -28M13 rev2 from Amersham
High quality sequence stop: 438.
Location/Qualifiers
1.475
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/dev_stage="4 weeks"
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Best Local Similarity 76.0%;
Matches 38; Conservative
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                                                                                                                             house mouse.
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FEATURES

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Search completed: Thu Aug 21 14:17:25 1997 Job time: 1043 secs.
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Bukaryotae; mitochondrial eukaryotes; Alveolata; Apicomplexa; Bukaryotae; mitochondrial eukaryotes; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

1 (bases 1 to 289)
1 (bases 1 to 289)
2 Dame, J.B., Arnot, D.E., Bourke, P., Chakrabarti, D., Christodoulou, Z., Coppel, R., Coman, A., Craig, A., Fischer, K., Foster, J., Goodman, N., Hinterberg, K., Holder, A.A., Holt, D., Kemp, D., Lanzer, M., Lim, A., Newbold, C., Ravetch, J.Y., Reddy, G. R., Rubio, J., Schuster, S. M., Su, X.-Z., Thompson, J.K., Vital, F., Wellems, T. E. and Werner, E. Current status of the Plasmodium falciparum genome project

By7001675
                                                                                                                                                                                                                                                                                                                                              /note="Vector: Lambda ZAP II; Site_1: ECOR I; Site_2: Xho I; PolyA+ RNA, from asynchronous blood stage parasites of the Da2 isolate cultured in vitro, was reverse transcribed using an oligo dr-Xho I primer. Second strand was prepared using RNase H and DNA polymerase I. ECOR I adapters were ligated to the cDNA, and it was digested with Xho I. Prepared fragments were ligated into ECOR I + Xho I digested lambda ZAP II vector."

/clone="PF2149C"
/clone="PF2149C"
/lab_host="Ecoli XL-1 blue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 289 bp mRNA EST 18-NOV-1996
Nd2.1, Debopam Chakrabarti Plasmodium falciparum CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
  Current status of the Plasmodium falciparum genome project
Mol. Biochem. Parasitol. 79, 1-12 (1996)
97001675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 24; DB 1; Length 228; Pred. No. 3.33e-05; 0; Mismatches 20; Indels
                                                                                       Contact: Debopam Chakrabarti
Department of Molecular Biology and Microbiology
University of Central Florida
Orlando, FL 32816-2360
Tel: 407 384 2061
Fax: 407 384 3095
Email: dchak@pegasus.cc.ucf.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Debopam Chakrabarti
Department of Molacular Biology and Microbiology
University of Central Florida
Orlando, FL 32816-2360
Tel: 407 384 2061
Fax: 407 384 3095
Emai: dchaképegasus.cc.ucf.edu
Seq primer: T3.
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9
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                                                                                                                                                                                                                                                                                                                               /strain="Dd2"
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Bost Local Similarity 68.8%;
Matches 44; Conservative
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/note="Vector: Lambda ZAP II; Site_1: ECOR I; Site_2: Xho I; PolyA+ RNA, from asynchronous blood stage parasites of the Da2 isolate cultured in vitro, was reverse transcribed using an oligo dT-Xho I primer. Second strand was prepared using RNase H and DNA polymerase I. ECOR I adapters were ligated to the CDNA, and it was digested with Xho I. Prepared fragments were ligated into ECOR I Xho I digested lambda ZAP II vector. "Clone="PF2232C" / Clone="PF2232C" / Lambda ZAP II vector." | Abb_host="E. coli XL-1 blue" | Lab_host="E. coli XL-1 blue" | Lab_host=
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Pred. No. 1.98e-06;
0; Mismatches 25; Indels
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Location/Qualifiers
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Best Local Similarity 66.7%;
Matches 50; Conservative
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US-08-320-157-9.rag

(TM)
(MZ)  -   -   -     -

Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Wed Aug 20 11:04:54 1997; MasPar time 5.42 Seconds 445.465 Million cell updates/sec Run on:

not generated. Tabular output >US-08-320-157-9 (1-211) from US08320157.pep 1554 Description: Perfect Score:

1 MASGQGPGPPRQECGEPALP.....LVVLGVVLLGQFVVRRFFKS 211 Scoring table:

Sequence:

PAM 150 Gap 11

96640 segs, 11439865 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

i:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 a-geneseq27

scale 0.230 Variance 141.390; Mean 32.557; Statistics

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description	Pred. No.
1	1554	100.0	211	20	W03669	Bak-2 protein.	8 166-138
7	1554	100.0	211	13	R77877		8 16e-138
m	1529	98.4	211	13	R77876	Human Cdn-1.	2.326-135
4	1529	98.4	211	20	W03668	Bak protein.	2.32e-135
Ŋ	1529	98.4	211	17	R81451	Bcl-Y apoptosis-relat	2.32e-135
ø	1136	73.1	152	13	R77879		6.78e-97
7	1001	68.3	141	13	R77880	Human Cdn-1(71-211).	1.38e-89
ω	880	9.95	116	13	R77881	Human Cdn-1(96-211).	5.18e-72
σ	275	17.7	232	13	W01020	Apoptosis-blocking pr	9.24e-15
10	271	17.4		13	R68884	Chicken lymphoid BCL-	2.11e-14
11	264	17.0		13	R68887	Human thymus BCL-XL.	8.96e-14
12	264	17.0	233	20	W05821	Bcl-XL protein.	8.96e-14
13	262	16.9		13	W01019	Apoptosis-blocking pr	1.35e-13
14	262	16.9		19	W01018	Apoptosis-blocking pr	1.35e-13
15	260	16.7		13	R71405	Human bcl-2 beta prot	2.04e-13
16	260	16.7		13	R68886	Human thymus BCL-2.	2.04e-13
17	260	16.7		13	R70332	Human bcl-2 protein.	2.04e-13
18	260	16.7		13	R71404	Human bcl-2 alpha pro	2.04e-13
19	260	16.7	239	σ	R47344	Human oncodene bcl-2	2.04e-13
20	260	16.7	239	~	P80987	Sequence of bcl-2-alp	2.04e-13

2.04e-13	2.04e-13	9.35e-11	4.71e-10	8.62e-10	2.88e-09	7.82e-09	1.34e-06	3.61e-05	7.02e+00	9.81e+00	1.16e+01	1.16e+01	1.16e+01	1.37e+01	1.61e+01	1.61e+01	1.61e+01	1.61e+01	1.61e+01	1.61e+01	3.09e+01	3.09e+01	3.09e+01	3.09e+01
Human bcl-2 protein.	Bcl-2 oncogene produc	Sequence of bcl-2-bet	Apoptosis-blocking pr	Murine Bax protein.	Human Cdn-3.	Human Bax protein.	Human mcl-1 gene prod	Human thymus BCL-X1.	Deduced sequence enco	Human thymus BCL-XS.	Human IFG-1 receptor.	Human type I insulin-	IGF-1 receptor.	Duffy blood group gpD		IGF-I receptor 957A v	IGF-I receptor 950X v	IGF-I receptor 1003A	IGF-I receptor 943A v	IGF-I receptor.	ACT-4-h-1 receptor se	Insecticidal protoxin	Peripheral nervous sy	Peripheral nervous sv
R70331	R42312	P80988	W01021	R71407	R77878	R71406	R68814	R68885	R76996	R68888	R60795	R91429	R95244	R73955	R11516	R63125	R63124	R63126	R63123	R63122	R79904	R48678	R99639	R92317
13	œ	Н	19	13	13	13	12	13	14	13	11	17	17	14	7	11	11	11	11	11	15	თ	18	18
239	239	202	229	192	88	192	320	63	277	170	1367	1367	1367	338	740	1337	1337	1337	1337	1367	277	1157	1984	1989
٠	٠	•	14.3	14.1	13.7	13.4	11.7	10.6	6.3	6.2	6.1		6.1	0.9		٠	0.9		0.9			•	5.7	5.7
260	260	230	222	219	213	208	182	165	86	96	95	95	95	94	93	93	93	93	93	6 6	88	83	83	88
21	22	23	24	25	56	27	28	59	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

protein

State of the sequence represents a bcl-1 homologue which

This Bak-2 protein sequence represents a bcl-1 homologue which

Interacts with Epstein-Bar virus (EBV) early lytic cycle BHRF1

Crossin and is capable of modulating apoptosis. The protein may

Exportein, and is capable of modulating apoptosis. The protein may

Crossin in a new virucide drug screening method, which involves

Combination of Bak-2 protein and a viral protein (e.g. EBV BHRF1),

Combination of Bak-2 protein and monitoring for disruption of the

interaction, e.g. by co-precipitation, protein interactive trapping

or ELISA. Interaction of Bak-2 and viral proteins allows viral

creplication or latency in the absence of apoptosis. Compounds which

inhibit the interaction may be used as virucide, antitumour or ning for anti-viral agents – by detecting the ability of an to disrupt the interaction of a Bak protein and a viral Bak-2 protein. Haman; Bak-2; apoptosis; latency; virus replication; Epstein-Bak-2; apoptosis; latency; virus replication; Epstein-Barr virus; BHRF1; fusion protein; epitope tag; drug screening; co-precipitation; ELISA; immunoassay; antibody; protein interactive trapping; virucide; antitumour; diagnostic. WO9633416-A1. Ä. 19-APR-1996; U05639. 20-APR-1995; US-426529. (LXRB-) LXR BIOTECHNOLOGY INC. RESULT 1 ID W03669 standard; Protein; 211 22-FEB-1997 (first entry) Barr PJ, Kiefer MC; WPI; 96-485886/48. N-PSDB; T42139. Screening for anti-vir diagnostic agents 211 AA 24-OCT-1996 Sequence W03669; agent 

ö 0; Gaps Score 1554; DB 20; Length 211; Pred. No. 8.16e-138; 0; Mismatches 0; Indels 0 Similarity 100.0%; S11; Conservative Local Sim. 211; C Query Match Best Loc Matches

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 vtlplqpsstmgqvgrqlaiigddinrrydsefqtmlqhlqptaenayeyftkiasslfe
                                          sginwgrvvallgfsyrlalhiyqrgltgflgqvtrfvvdfmlhhciarwiaqrggwvaa

        masggggppprgecgepalpsaseegvadteevfrsyvfyhhggegeaegaaapadpem

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 VILPLOPSSTMGQVGRQLAIIGDDINRRYDSEFQTMLQHLQPTAENAYEYFTKIASSLFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sginwgrvvallgfsyrlalhiyqrgltgflgqvtrfvvdfmlhhclarwiaqrggwvaa
                     VTLPLOPSSTMGQVGRQLAIIGDDINRRYDSEFQTMLQHLQPTAENAYEYFTKIASSLFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV; autoimmune disease; reperfusion injury; hepatitis, osteoporosis; shock; lymphoma; eczema. Homo sapiens.
                                                                                                                                                                                     Cdn-2; apoptosis modulator; adoptive immunotherapy; therapy; HIV; autoimmune disease; reperfusion injury; hepatitis, osteoporosis; shock; lymphoma; eczema. Homo sapiens. W09515084-A.
                                                                                                                                                                                                                                                                                                                                                                                   Cdn-2 CDNA was isold. from a human placental genomic library using a 950 bp fragment of Cdn-1 CDNA. Expression of Cdn-2 in mouse progenitor B-cell FL5.12 cells decreased IL-3-induced apoptosis. The Cdn-2 protein displayed 97% amino acid identity with Cdn-1 (R77876).
Sequence 211 AA;
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                                                                                Inlgngpilnvlvvlgvvllggfvvrrffks 211
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R77877 standard; Protein; 211
R77877;
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                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                        30-NOV-1994; U13930.
30-NOV-1993; US-160067.
07-OCT-1994; US-320157.
                                                                                                                                                                                                                                                                                                   Kiefer MC;
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WPI; 95-215106/28.
N-PSDB; Q95493.
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                                                                                                                                                                      21-NOV-1995
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                                                                                                                                                                                    N-PSDB; 095492.
New nucleic acid sequences encoding Cdn apoptosis modulators - and related vectors, transformed cells, proteins and antibodies, useful or diagnosis and treatment e.g. of HIV infection, reperfusion injury
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                                                                                                                                                                                                                                                                                                                     Can-l cDNA was isolated from a human heart cDNA library using a previously isolated clone as probe. Recombinant Can-1 was produced in Sf9 and human colon adenocarcinoma HT29 cells. Expression of cdn-1 in WI-L2 lymphoblastoid cells resulted in increased cell survival in response to anti-Fas-mediated apoptosis.
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Epstein-Barr virus; BHRF1; fusion protein; epitope tag;
drug screening; co-precipitation; ELISA; immunoassay; antibody;
protein interactive trapping; virucide; antitumour; diagnostic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1529; DB 13; Length 211;
Pred. No. 2.32e-135;
5; Mismatches 1; Indels 0
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Disclosure; Fig 1; 24pp; English.
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W03668 standard; Protein; 211
                                                                                                        (LXRB-) LXR BIOTECHNOLOGY INC.
Barr PJ, Kiefer MC;
WPI; 95-215106/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98.4%; silarity 97.2%; Conservative
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19-APR-1996, U05639.
20-APR-1995, US-426529.
(LXRB-) LXR BIOTECHNOLOGY IN
Barr PJ, Kiefer MC;
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22-FEB-1997 (first entry)
                                                     30-NOV-1993; US-160067.
07-OCT-1994; US-320157.
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WPI; 96-485886/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         211 AA;
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08-JUN-1995.
30-NOV-1994;
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Homo sapiens.
WO9515084-A.
08-JUN-1995.
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WO9515084-A.
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    which
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Bcl-Y protein (R81451) is a member of the Bcl-2 family and can induce apoptosis in cells and function as a negative regulator of Bcl-2 function. Bcl-Y mRNA was detected in all human tumour cell lines examined and is also widely expressed in primary human tissues. It can be obtd. by expression of a full-length cDNA clone (T17375) in pref. mammalian host cells. Bcl-Y can be used to develop prods. for treating disorders associated with inappropriate cell proliferation or cell death, and to raise antibodies used for
                                                                             Gaps
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replication or latency in the absence of apoptosis. Compounds inhibit the interaction may be used as virucide, antitumour or
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Bcl-Y; apoptosis; cell proliferation; cell death; diagnosis;
                                                       Length 211;
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                                                      Score 1529; DB 20;
Pred. No. 2.32e-135;
5; Mismatches 1;
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Local Similarity 97.2%; Pred. No. 2.32e-135;
les 205; Conservative 5; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                      /label- C-terminal_domain
/note- "putative membrane localisation sequence"
WO9605232-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the diagnosis or monitoring of such disorders
                                                                                                                                                                                                                                              181 LNLGNGPILNVLVVLGVVLLGQFVVRRFFKS 211
                                                                                                                                                                                                                                  181 lnlgngpilnvlvvlgvvllggfvvrrffks 211
                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
188..205
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R81451 standard; Protein; 211 AA.
                                                    Query Match
Best Local Similarity 97.2%;
Matches 205; Conservative
                                                                                                                                                                                                                                                                                                                        02-JUL-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                        22-FFB-1996.
09-AUG-1995; U10103.
09-AUG-1994; US-287427.
11-CCT-1994; US-321071.
(IMMU ) IMMOUNGEN INC.
Chittenden ID;
WPI: 96-139648/14.
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                    diagnostic agents.
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New nucleic acid sequences encoding Cdn apoptosis modulators - and related vectors, transformed cells, proteins and antibodies, useful or diagnosis and treatment e.g. of HIV infection, reperfusion injury
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Expression of Cdn-1 in WI-L2 lymphoblastoid cells resulted in increased cell survival in response to anti-ras-mediated apoptosis. Deletion of the N-terminal 59 amino acids of Cdn-1 only slightly decreased this activity, suggesting that small, truncated Cdn-1 Sequence 152 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV;
                                                                                                                                                                                                                                                                                                                         Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV autoimmune disease; reperfusion injury; hepatitis, osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          autoimmune disease; reperfusion injury; hepatitis, osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 73.1%; Score 1136; DB 13; Length 152; Local Similarity 97.4%; Pred. No. 6.78e-97; les 148; Conservative 4; Mismatches 0: Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R77880 standard; Protein; 141 AA
                                                                                                                                                                                                        T 6
R77879 standard; Protein; 152
R77879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-NOV-1994; U13930.
30-NOV-1993; US-160067.
07-OCT-1994; US-320157.
(LXRB-) LXR BIOTECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (LXRB-) LXR BIOTECHNOLOGY INC.
                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                            shock; lymphoma; eczema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              shock; lymphoma; eczema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-NOV-1994; U13930.
30-NOV-1993; US-160067
07-OCT-1994; US-320157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Barr PJ, Kiefer MC;
WPI; 95-215106/28.
                                                                                                                                                                                                                                                                                                     Human Cdn-1(60-211)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human Cdn-1(71-211)
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antibodies, useful in assay and for control of cell death in e.g. antibodies, useful in assay and for control of cell death in e.g. neuronal cells, lymphocytes and cancers
claim 4; Page 87; 127pp; English.
This protein may be expressed recombinantly, particularly with pcmV plasmids as vectors for expression in mammalian cell cultures.
The protein has particular application in cancer cells (failure of programmed cell death (PCD)) or neurodegenerative and autoimmune diseases
                                                                                                                                                                                                                                                                                                Chinadural G;

WPI; 96-427055/43.

WPI; 96-427055/43.

WPI; 96-427055/43.

WPI; 96-427055/43.

WRIGH acids encoding apoptosis regulating proteins - useful for diagnosing and treating immune disorders, malignancies, etc.

Example 8; Page 34-35; 60pp; English.

CC The 80-6 mutant (W01020) of the bcl-2 oncogene product (W01018)

CC lacks amino acids 80-86 of the native protein. This and other

CC Bcl-2 mutants (see also W0109-21) were used in a two hybrid assay

CC examine the interactions between Bcl-2 and novel apoptosis-

CC committing proteins will, Nip2 and Nip3 (W00997-99). 2 Motifs

CC (W01003-04) on Bcl-2 were identified that are essential for

interaction with the Nip proteins. These motifs show homology

CC to motifs (W01005-06) identified on the adenovirus E1B 19K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48 ffssgpghtphpaasr-dpvartsplgtpaapgspvppvvhltlrgagddfsrryrrdfa 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   107 emssqlhltpftargcfatvveelfrdgvnwgrivaffefggvmcvesvnremsplvdni 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95 TMLQHLQPTAENAYEYFTKIASSLFESGINWGRVVALLGFSYRLALHIYQRGLTGFLGQV 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neurodegenerative disease; autoimmune disease; Parkinson's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40 FYHHQQEQEAEGAAAPADPEMVTLPLQPSSTMG-QVGR--QLAI--IGDDINRRYDSEFQ
                   18-DEC-1996 (first entry)
Apoptosis-blocking protein Bcl-2 mutant 80-6 (del80-86).
Apoptosis-regulating protein; Bcl-2; oncogene;
adenovirus ElB 19K protein; cell death; cancer; tumour;
immune disorder; diagnosis; therapy; Bipla; Bipl3; Bip5; NIp1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amylotrophic lateral sclerosis; multiple sclerosis; oncogene. Gallus domesticus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New poly-nucleotide encoding new poly-peptide(s) that modify
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chicken lymphold BCL.X.
Chicken; bird; fowl; BCL.X; apoptosis; cell death; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 275; DB 19; Length 23
Pred. No. 9.24e-15;
41; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              167 alwmteylnrh-lhtwiqdnggwdafvel-ygpsmrpl 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : ::::: | : | | : | | :: | : | : | 155 TRFVVDFMLHHCIARWIAQRGGWVAALNIGNGPILNVL 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thompson CB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R68884 standard; Protein; 190 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47; Conservative
                                                                                                                                                                                                                                   21-MAR-1996; 104542.
21-MAR-1995; US-408095.
(UYSL-) UNIV ST LOUIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-04N-1293, 007089, 22-UN-1994; 007089, 22-UN-1993; US-081448. (ARCH-) ARCH DEV CORP. (UNIT) UNIV MICHIGAN. Bolse LH, Nunez G, ThWPI; 95-052079/07.
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                                                                                                                                                                                         EP-733706-A2.
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                                                                                                                                             Nip2; Nip3.
                                                                                                                                                                                                                    25-SEP-1996
                                                                                                                                                                      Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                           71 MGQVGRQLAIIGDDINRRYDSEFQTMLQHLQPTAENAYEYFTKIASSLFESGINWGRVVA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 mlqhlqptaenayeyftkiatslfesginwgrvvallgfgyrlalhvyqhgltgflggvt 60
                                                                                                                                                                                                                                                                                                                                                                               1 mgqvgrqlaiigddinrrydsefqtmlqhlqptaenayeyftkiatslfesginwgrvva 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  related vectors, transformed cells, proteins and antibodies, useful or diagnosis and treatment e.g. of HIV infection, reperfusion injury
                        related vectors, transformed cells, proteins and antibodies, useful or diagnosis and treatment e.g. of HIV infection, reperfusion injury
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig.11; 66pp; English.
Expression of Cdn-1 in WI-L2 lymphoblastoid cells resulted in increased cell survival in response to anti-Fas-mediated apoptosis. Truncated Cdn-1 derivatives given in R77879-81 were used to test the effects of deleting the N-terminal sequences of Cdn-1
                                                                                     Disclosure; Fig.11; 66pp; English.

Expression of Cdn-1 in WI-L2 lymphoblastoid cells resulted in increased cell survival in response to anti-Fas-mediated apoptosis. Deletion of the N-terminal 70 amino acids of Cdn-1 improved this activity, suggesting that small, truncated Cdn-1 molecules may be
nucleic acid sequences encoding Cdn apoptosis modulators - and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV autoimmune disease; reperfusion injury; hepatitis, osteoporosis; shock; lymphoma; eczema.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid sequences encoding Cdn apoptosis modulators
                                                                                                                                                                                                                                                                                    Length 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56.6%; Score 880; DB 13; Length 116; Larity 96.6%; Pred. No. 5.18e-72; Conservative 4; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                  Score 1061; DB 13;
Pred. No. 1.38e-89;
4; Mismatches 0;
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30-NOV-1994; U13930.
30-NOV-1993; US-160067.
07-OCT-1994; US-320157.
(LXRB-) LXR BIOTECHNOLOGY INC.
BARY PJ. KARÉER MC;
WPI; 95-215106/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 vlvvlgvvllggfvvrrffks 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               191 VLVVLGVVLLGQFVVRRFFKS 211
                                                                                                                                                                                                                                                                               Match 68.3%;
Local Similarity 97.2%;
les 137; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-NOV-1995 (first entry)
                                                                                                                                                                                                                therapeutics.
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ses 112; Conser
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WO9515084-A.
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07-NOV-1996.
02-MAY-1996; U06203.
                                                                                                                                                                                                                                                                             "BH2 domain"
                                                                                                                                                                                           "BH1 domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       June CH, Thompson
WPI; 96-506159/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 233 AA;
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WPI; 96-427055/43.
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EP-733706-A2.
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WO9634956-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70 slevheivrasdvrgalrdagdefelryrrafsdltsglhitpgtaygsfegvvnelfhd 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 gvnwgrivaffsfggalcvesvdkemrvlvgrivswmttyltdh-1dpwigenggwvrta 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 TLPLQPSSTMGQVGRQLAIIGDDINRRYDSEFOTMLQHLQPTAENAYEYFTKIASSLFES 121
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Human; bc1-XL; T-lymphocyte; cell death; BH1 domain; BH2 domain;
Bc1-2 homology domain; gene therapy; HIV; AIDS; antisense;
immune disorder; autoimmune disease; graft rejection;
(premature PCD), e.g. Parkinson's disease, amylotrophic lateral sclerosis and multiple sclerosis.
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Pred. No. 8.96e-14;
37; Mismatches 46; Indels 7
                                                                                                                                                                                       Length 190;
                                                                                                                                                                             Score 271; DB 13; Length 19
Pred. No. 2.11e-14;
36; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T 11
R68887 standard; Protein; 233 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Boise LH, Nunez G, Thompson CB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W05821 standard; Protein; 233 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 17.0%;
Best Local Similarity 28.0%;
Matches 33; Conservative
                                                                                                                                                                             Match 17.4%;
Local Similarity 28.1%;
les 34; Conservative
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30-MAR-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-AUG-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-JUN-1994; U07089.
22-JUN-1993; US-081448.
(ARCH-) ARCH DEV CORP.
(UNMI ) UNIV MICHIGAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human thymus BCL-XL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo saptens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9500642-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 L 181
                                                                                           Sequence
                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R68887;
                                                                                                                                                                                                                                                                             Matches
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ID WO
AC WO
DT 30
DE BC
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Inducing or preventing death of T cells by bcl-XL protein regulation
The four case survival of HIV infected cells or to
The wised to increase survival of HIV infected cells or to
The wise of the camene responses in immune diseases
Disclosure; Page 52-53; 76p; English.
This is the sequence of a human bcl-XL protein, which protects
Thymphorytes against cell death. A splice variant form, bcl-XS,
acks a stretch of 63 amino acids, and is a dominant negative
cequlator of bcl-XL function. The gene may be modified to
facilitate interaction with antagonistic Bad protein, by modification of the
Bcl-2 homology domains BHI and/or BH2. The bcl-XL gene may be
intraduced into T-cells in vivo or ax vivo via gene transfer using
a vector for HIV infection gene therapy, to ougment intracellular
bcl-XL protein levels and protect from cell death. A corresponding
contisence of the correspondence contisence of the cape of the corresponding contisence of the corresponding contisence of the corresponding contisence cell death (e.g. apoptosis) and
contisence of correspondence cell death (e.g. apoptosis) and
corresponding the immune response in a T-lymphocyte population.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83 maavkqalreagdefelryrrafsdltsqlhitpgtayqsfeqvvnelfrdgvnwgriva 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71 MGQVGRQLAIIGDDINRRYDSEFQTMLQHLQPTAENAYEYFTKIASSLFESGINWGRVVA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143 ffsfggalcvesvdkemqvlvsriaawmatylndh-lepwiqenggwdtfvelygnna 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding apoptosis regulating proteins - useful for diagnosing and treating immune disorders, malignancies, etc.
Example 8: Page 33-34; 60pp; English.
The 42-8 mutant (W01019) of the Dc1-2 oncogene product (W01018)
lacks amino acids 42-48 of the native protein. This and other Bc1-2 mutants (see also W01020-21) were used in a two hybrid assay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-DEC-1996 (first entry)
Apoptosis-blocking protein Bcl-2 mutant 42-8 (del42-48).
Apoptosis-regulating protein; Bcl-2; oncogene; tancounts ElB 19% protein; cell death; cancer; tumour; immune disorder; diagnosis; therapy; BiplA; Bipl3; Bip15; NIP1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ~
graft-versus-host disease; apoptosis; adoptive immunotherapy. Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 264; DB 20;
Pred. No. 8.96e-14;
                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       n 13
W01019 standard; Protein; 232 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 28.0%;
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                                                                                                                   129..148
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21-MAR-1995; US-408095.
(UYSL-) UNIV ST LOUIS.
                                                                                                                                                                                                                                                                                                                                                                                      04-MAY-1995; US-435518.
07-JUN-1995; US-481739.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ARCH-) ARCH DEV CORP.
(USNA ) US SEC OF NAVY.
June CH, Thompson CB;
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US-08-320-157-9.rag

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/label- BH1_domain
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                                                                                                                                                                                                                                                                    Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Korsmeyer SJ
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                                                                                                                                                                                                                                                        tpaapgaaagpalspvppvvhlt--lrqagddfsrryrrdfaemssglhltpftargcfa 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APADPEMVILP-LQPSSTMGQVGRQLAIIGDDINRRYDSEFQTMLQHLQPTAENAYEYFT 112
                                                                                                                                                                                     tpaapgaaagpalspvppvvhlt--lrqagddfsrryrrdfaemssglhltpftargcfa 124
                                                                                                                                                                                                               APADPEMVTLP-LQPSSTMGQVGRQLAIIGDDINRRYDSEFQTMLQHLQPTAENAYEYFT 112
                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-MAR-1996; 104542.
21-MAR-1995; US-408095.
(UYSL-) UNIV ST LOUIS.
Chinnedural G:
WPI; 96-427055/43.
Nucleic acids encoding apoptosis regulating proteins - useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnosing and treating immune disorders, malignancies, etc.
Example 8; Page 32-33; 60pp; English.
The bcl2 oncogene product (W01018) enhances the survival of haematopoietic B and T cells by blocking apoptosis induced by divorse agents. Its activity is similar to that of the 19k protein (W01010) of adenovirus Elb. 3 Novel proteins. Bipla, Bipl3 and Bip5 (W01000-02), that specifically interact with W01019-21) shows the apoptosis-regulating Nip proteins (see also W00099-99) associate with Bcl-2 at specific sites (see also W0109-19) associate with Bcl-2 at specific sites (see also W01003-04) that show homology to motifs (W01005-06) on 19K.
              regulating proteins Nipi, Nip2 and Nip3 (W00997-99). The Nip Proteins were unable to interact with mutent 42-8. The site of deletion in this mutent corresponds to a motif (see also W01003) on BC1-2 essential for interaction with Nip proteins. A second binding motif (W01004) of BC1-2 was also identified, and both show homology to motifs (W01005-06) found on the 19K protein (W01010) of adenovirus Elb.
                                                                                                                                                                                                                                                                                                                                                                                  18-DEC-1996 (first entry)
Apoptosis-blocking protein Bcl-2.
Apoptosis-regulating protein; Bcl-2; oncogene;
adenovirus ElB 19k protein; cell death; cancer; tumour;
immune disorder; diagnosis; therapy; Bipla; Bipl3; Bip5; NIp1;
Nip2; Nip3.
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examine the interactions between Bcl-2 and novel apoptosis-
nulating proteins Nip1, Nip2 and Nip3 (W00997-99). The Nip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 262; DB 19; Length 239;
Pred. No. 1.35e-13;
37; Mismatches 57; Indels
                                                                                                                                    Length 232;
                                                                                                                                  Score 262; DB 19; Length 23; Pred. No. 1.35e-13; 37; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proteins"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label-Binding_motif
/note= "interacts with Bip proteins"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                     W01018 standard; Protein; 239 AA
                                                                                                                                                                                                                                                                                                          : ||| | ::| || : |
173 QRGGWVAALNLGNGPILNVL 192
                                                                                                                                                                                                                                                                                          184 dnggwdafvel-ygpsmrpl 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16.9%;
llarity 29.3%;
Conservative
                                                                                                                                  Match 16.9%;
Local Similarity 29.3%;
108 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label- Binding_motif
/note- "interacts with Bip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            106..112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    239 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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                                                                                                           Seguence
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Wethods for producing and identifying mutant bcl-2 proteins -
That lack death repressor activity and/or lacks binding to Bax.

For that lack death repressor activity and/or lacks binding to Bax.

By Disclosure; Page 40; 133pp; English.

The sequences given in R71404.05 represent the human bcl-2 alpha and complete and a proteins respectively. bcl-2 is encoded by a proto-oncogene and is capable of inhibiting apoptosis in many hematopoletic cell systems.

Col-2 is a 26 kD membrane-associated cytoplasmic protein and is thought coffunction by enhancing the survival of hematopoletic cell systems.

Col-2 is a 26 kD membrane-associated cytoplasmic protein and is thought coling rather than directly promoting proliferation of these cell cycle coling rather than directly promoting proliferation of these cell cycle types. bcl-2 has not been shown to directly promote cell cycle progression nor does it necessarily alter the dose reponse to limiting a late of protein, Bax. Overexpressed Bax accelerates apported; cell death concentrations of IL-3. bcl-2 has been shown to form heterodimers with also acts to counter the death repressor activity of bcl-2. Therefore, calso between bcl-2 and Bax determines cell survival or death components to be a proportic stimulus. The invention gives a mutant form of bcl-2 in which there is at least one amino acid substitution or deletion collowing an apoptotic stimulus. The invention gives a mutant form of bcl-2 in which there is at least one amino acid substitution of bcl-2 in usaful in cancer therapy, controlling contexpended to bcl-2 is useful in cancer therapy, controlling contexpended and diagnosis of immunodeficiency diseases, including Albert and element and diagnosis of immunodeficiency diseases, including Albert and element and ischaemic cell death.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3,
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                                                 132 tvveelfrdgvnwgrivaffefggvmcvesvnremsplvdnialwmteylnrh-lhtwig 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; bcl-2; alpha; beta; proto-oncogene; hematopoietic cell line; apoptosis; membrane-associated cytoplasmic protein; B cell; T cell; proliferation; cell cycle progression; Bax; apoptotic cell death; apoptosis; cytokino; death repressor; BHI; BH2; cancer therapy; hyperplasia; immunodeficiency disease; AIDS; neurodegeneration; ischaemic cell death.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 205;
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Pred. No. 2.04e-13;
37; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Represents Bax binding site"
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136..155
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                                                                                                                                                                                                                                                                                                                                                                                            T 15
R71405 standard; protein; 205
                                                                                                                                                                       191 dnggwdafvel-ygpsmrpl 209
                                                                                                                                                                                                                                                             173 QRGGWVAALNLGNGPILNVL 192
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Similarity 29.7%;
38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R71405;
30-OCT-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human bcl-2 beta protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-AUG-1993; US-112208.
25-MAY-1994; US-248819.
(UNIW ) UNIV WASHINGTON.
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113 KIASSLFESGINWGRVVALLGFSYRLALHIYQRGLTGFLGQVTRFVVDFMLHHCIARWIA 172 δ

191 dnggwyga 198 : ||||:| 173 QRGGWVAA 180 δy qq

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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Wed Aug 20 11:06:16 1997; MasPar time 6.19 Seconds 723.119 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-320-157-9 (1-211) from US08320157.pep 1554 1 MASGQGPGPPRQECGEPALP......LVVLGVVLLGQFVVRRFFKS 211 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

59021 seqs, 21210388 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

swiss-prot34
l:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11

Mean 47.039; Variance 90.944; scale 0.517 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Pred. No.	1.55e-29	1.34e-28	3.16e-28	9.72e-27	9.72e-27	8.18e-26	8.18e-26	1.25e-25	2.37e-20	4.87e-18	3.69e-17	7.38e-13	5.01e-13	5.09e-12	1.73e - 07	5.05e-07	1.46e-06	4.77e-03	5.81e-02	1.07e-01	1.07e-01
Description	APOPTOSIS REGULATOR B	REGULATOR	IS	PROTEIN BCL-2-BETA.	PROTEIN BCL-2-ALPHA.	PROTEIN BCL-2-BETA.	PROTEIN BCL-2 ALPHA.	PROTEIN BCL-2 ALPHA.	APOPTOSIS REGULATOR B	APOPTOSIS REGULATOR B	APOPTOSIS REGULATOR B	BAX PROTEIN, CYTOPLAS	INDUCED MYELOID LEUKE	HEMOPOIETIC-SPECIFIC	APOPTOSIS REGULATOR B	APOPTOSIS REGULATOR B	APOPTOSIS REGULATOR B	HEAT SHOCK PROTEIN HT	CYTOCHROME C OXIDASE	LOW-AFFINITY GLUCOSE	LOW-AFFINITY GLUCOSE
Π	BCLX_CHICK	BCL2_CHICK	BCLX_HUMAN	BC2B_HUMAN	BC2A_HUMAN	BC2B_MOUSE	BC2A_MOUSE	BCL2_RAT	BAXA_MOUSE	BAXA_HUMAN	BAXB_HUMAN	BAXD_HUMAN	MCL1_HUMAN	HSA1_MOUSE	EAR_ASFE4	EAR_ASFB7	EAR_ASFM2	HTPG_BACSU	COX3_CAEEL	HXT3_YEAST	HXT4_YEAST
8			7	ч	-	ч	<del></del> 1	Н	Н	<del>, ,</del>	Н	Н	ဖ	Ŋ	m	m	m	Ŋ	~	Ŋ	S
Query Match Length DB	190	233	233	202	239	199	236	236	192	192	218	143	350	172	179	179	179	626	255	567	216
Query Match	17.4	17.1	17.0	16.5	16.5	16.2	16.2	16.1	14.2	13.4	13.1	11.5	11.5	11.1	ю. Э	9.1	8 6.8	7.4	6.9	6.8	9.8
Score	271	266	264	256	256	251	251	250	221	208	203	178	179	173	145	142	139	115	101	105	105
Result No.	12	m	4	N.	Φ.	7	ω	თ	10	11	12	13	14	15	16	17	18	19	20	21	22

1.11e+00 1.48e+00 1.96e+00 1.96e+00 1.96e+00 1.96e+00 2.59e+00 4.49e+00 4.49e+00 4.49e+00	SOO ODDUSZ	CW41,YEAST HST6_CANAL YNX6_OAEEL YUC9_YEAST AR56_SCHPO IGIR_HUMAN RRPO_CRV RRPO_CRV MLEF_HUMAN HXT1_YEAST PNA1_SCHPO ALIGNMENTS	2 833 3 1833 3 1833 3 1833 3 1833 3 1832 11 1 865 5 5 6 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6	4 4 4 4 5 7 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	34 34 35 37 37 37 37 44 44 44 45 45 47 47 47 47 47 47 47 47 47 47 47 47 47
	HYPOTHETICAL 95.4 KD ARG11 PROTEIN PRECURS	YJC9_YEAST AR56_SCHPO	822 1 885		& & & & & & & & & & & & & & & & & & &
1.96e+00 1.96e+00	HYPOTHETICAL 51.6 KD HEXOSE TRANSPORTER 2.	YNX6_CAEEL KHT2_KLULA	1 462 1 566		36 37
1.11e+00 1.48e+00		CW41_YEAST HST6_CANAL	2 833 2 1323		3.4 3.5
1.11e+00 1.11e+00	HIGH AFFINITY HEXOSE HIGH AFFINITY HEXOSE	HXT6_YEAST HXT7_YEAST	570		3 80
8.37e-01 1.48e+00	SYSTEM, FR ON STARVAT	PTFB_MYCGE CSTA_ECOLI	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		31
	HEXOSE TRANSPORTER HX HEXOSE TRANSPORTER HX	HXT9_YEAST	567	000	8 6 6 7 7 7
.94e-		RRPO_TBSVC YAD7_SCHPO	6 817 4 527		27
.61	THREONINE SYNTHASE (E HEXOSE TRANSPORTER HX	THRC_PSEAE HXT8_YEAST	6 470		25
1.44e-01	GOP PROTEIN.	GOP_BPP4	7 133		23

	. · · · · · · · · · · · · · · · · · · ·	BCL-X. GALLUS GALLUS (CHICKEN). EUKARYOTA, METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;	., DING L., LINDSTEN T.,	74:597-608(1993). FUNCTION: DOMINANT REGULATOR OF APOPTOTIC CELL DEATH. TISSUE SPECIFICITY: HIGHEST EXPRESSION IN ORGANS WITH LYMPHOLD DEVELOPMENT.		; 7874E430 CRC32; Score 271; DB 1; Length 190; Pred. No. 1.55e-29; 36; Mismatches 49; Indels 2; Gaps 2	70 slevheivrasdvrqalrdaqdefelryrrafsdltsqlhitpgtayqsfeqvnelfhd 129 	<pre>gvnwgrivaffsfggalcvesvdkemrvlvgrivswmttyltdh-ldpwiqenggwvrta 188  :    :  :: :  </pre>	
190 AA.	ATE) PDAT		3. E. 3. B.	TOT	41LY	CRC DB DB .55e	ltsg : : MLQH	swmt : RFVV	
19(	UPD.	3RAT?	EMA SON (	APO]	FA	2430 71; 5. 1	fsd.   SFQTI	rivs ::	
PRT;	TED) SEQUENCE ANNOTATIC	TA; VERTEB	A M., POST G., THOMPS	74:597-608(1993). TISSUE SPECIFICITY: HIGHEST EXPRESSION IN LYMPHOID DEVELOPMENT.	33	<b>≩</b>	defelryrra  :::    DDINRRYDSE	vdkemrvlvg :: ::: YQRGLTGFLG	
STANDARD;	31, CREA 31, LAST 31, LAST OR BCL-X.	ICKEN). A; CHORDA	LEZ-GARCI	993). INANT REGICITY: HI	ELONGS TO 0899; 37. BCL2.	190 AA; 21467 MW; 17.4%; S: Similarity 28.1%; P: 34; Conservative 3	vrgalrdag   :   VGRQLAIIG	fggalcves  : :  FSYRLALHI	
ST	REL. REL. REL.	(CH	FROM N.A. 93364977. ., GONZAI	DOM DOM DEVE	G51 G51 A475 080;	190 AA; ilarity Conserv	rasd :: TMGQ	affs  :::  ALLG	
T 1 BCLX_CHICK	OCTORS (REL. 31, CREATED) 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE) 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE) APOPTOSIS REGULATOR BCL-X.	BCL-X. GALLUS GALLUS (CHICKEN). EUKARYOTA; METAZOA; CHOR GALLIFORMES.	11) MEDUENCE FROM N.A. MEDUELINE; 93364977. BOISE L.H., GONZALEZ-GARCIA M., POSTEMA C.E., TURKA L.A., MAO X., NUNEZ G., THOMPSON C.B.;	CELL 74:597-608(1993)!- FUNCTION: DOMINANT R -!- TISSUE SPECIFICITY: LYMPHOID DEVELOPMENT	-1- SIMILAKIIY: BELONGS T EMB1; Z23110, G510899; PIR; A47537; A47537. PROSITE; PS01080; BCL2. APOPTOSIS.	ENCE atch cal	70 slevheiv :  :: 62 TLPLQPSS	130 gvnwgriv  :    :  122 GINWGRVV	189 1 189
RESULT ID B						SQ SEQUI	Db Qy	Db	qq

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233 AA.

PRT;

STANDARD;

RESULT 2 ID BCLX\_RAT

181 L 181

δy

TRANSMEMBRANE; MITOCHONDRION.

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APOPTOSIS;
       SCHEFFF
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EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;
GALLIFORMES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   maavkqalreagdefelryrrafsdltsqlhitpgtayqsfeqvvnelfrdgvnwgriva 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71 MGQVGRQLAIIGDDINRRYDSEFQTMLQHLQPTAENAYEYFTKIASSLFESGINWGRVVA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BIOCHIM. BIOCHUS. ACTA 1132:109-113(1992).

1- FUNCTION: PROLONGS THE SURVIVAL OF HEMATOPOIETIC CELLS IN THE ABSENCE OF REQUIRED GROWTH FACTORS AND ALSO IN THE PRESENCE OF VARIOUS STIMULI INDUCING CELLULAR DEATH. BLOCKS APOPTOSIS. MIGHT FUNCTION IN AN ANTIOXIDANT PATHWAY TO PREVENT APOPTOSIS. MIGHT FUNCTION IN AN INTOXIDANT PATHWAY TO PREVENT APOPTOSIS AT SITES OF FREE RADICAL GENERATION SUCH AS MITOCHONDRIA.

--- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE

(BY SIMILARITY: EXPRESSED IN A VARIETY OF TISSUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 ffsfggalcvesvdkemqvlvsriaswmatylndh-lepwiqenggwdtfvdlygnna 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SHOWN HERE) AND
                                                                                                                                    RATTUS NORVEGICUS (RAT).
EUKARXOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                           MICHABLIDIST.M.;
SUBMITTED (DEC-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
SUBMITTED (DEC-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
-1- FUNCTION: DOMINANT REGULATOR OF APOPTOTIC CELL DEATH.
-1- ALTERNATIVE PRODUCTS: TWO ISOFORMS, BCX-X(L) (SHOWN HERE BCL-X(S), ARE DERIVED BY ALTERNATIVE SPLICING.
-1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
R EMBL; X82537; GG07177; -.
APOPTOSIS; ALTERNATIVE SPLICING.
-1 APOPTOSIS; ALTERNATIVE SPLICING.
-1 VARSPLIC 126 188 MISSING (IN BCL-X(S)).
SEQUENCE 233 AA; 26130 MW; E0589815 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 268; DB 1; Length 233;
Pred. No. 5.65e-29;
37; Mismatches 46; Indels
                   01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
10-CCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
APOPTOSIS REGULATOR BCL-X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
APOPTOSIS REGULATOR BCL-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         233 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE, 92375724.
EGUCHI Y., EWERT D.L., TSUJIMOTO Y.;
NUCLEIC ACIDS RES. 20:4187-4192(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; D11382; G222794; -
EMBL; D11381; G222794; JOINED.
EMBL; Z11961; G62970; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 28.0%;
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A37332; A37332.
PIR; S24390; S24390.
PROSITE; PS01080; BCL2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE; 92379084.
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BCL2_CHICK
Q00709;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83
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SHEED COOKERER BOOOKE HER HOUSE SHEET HOUS
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                                                                                                                                                                                                        117 pftahgrfvavveelfrdgvnwgrivaffefggvmcvesvnremsplvdniatwmteyln 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83 maavkqalreagdefelryrrafsdltsqlhitpgtayqsfeqvvnelfrdgvnwgrlva 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     143 ffsfggalcvesvdkemqvlvsriaawmatylndh-lepwiqenggwdtfvelygnna 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E -> S (IN REF. 2).
GSAAASEVPPAEGLRP -> ARLLLVRCPRLRGCA
                                                                                                                                                          ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                           Length 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BOISE L.H., GONZALEZ-GARCIA M., POSTEMA C.E., DING L.,
LINDSTEN T., TURKA L.A., MAO X., NUNEZ G., THOMPSON C.B.;
CELL 74:597-608(1993).
                                                                                                                       Score 266; DB 1; Length 233
Pred. No. 1.34e-28;
42; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 17.0%; Score 264; DB 1; Length 233 Local Similarity 28.0%; Pred. No. 3.16e-28; Pred. S3; Conservative 37; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APOPTOSIS, ALTERNATIVE SPLICING.
126 188 MISSING (IN BCL-X(S)).
CONFLICT 70 70 G -> A (IN G510901).
SEQUENCE 233 AA; 26049 WW, 57C67491 CRC32;
                                               (IN REF. 2).
H -> T (IN REF. 2).
G -> V (IN REF. 2).
V; 3376502C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                     233 AA
    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                            177 rh-lhnwiqdnggwdafvelygns 199
                                                                                            25687 MW;
                                                                                                                       Query Match
Best Local Similarity 28.5%;
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APOPTOSIS REGULATOR BCL-X.
                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
    228
64
82
                                                          121
139
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                                                                                            233 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93364977
               64
67
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Q07817:
TRANSMEM
CONFLICT
CONFLICT
                                                                            CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE;
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                                                             CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- ALTERNATIVE PRODUCTS: TWO FORMS OF BCL-2: ALPHA, AND BETA, ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THEY ONLY DIFFER AT THEIR C-TERMINAL ENDS.
-i- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
PMBL; M19395; G173395; ALT_SEQ.
PIR; B29409; TWUUB1.
PIR; D37332; D37332.
                                                                                                                                                                                                                                                             EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS01080; BCL2, PROSITE; PS01080; BCL2, PROTO-ONCOGENE; APOPTOSIS; ALTERNATIVE SPLICING; MEMBRANE; MITOCHONDRION; CHROMOSOMAL TRANSLOCATION. SEQUENCE 205 AA; 22311 MW; ED321E5E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 16.5%; Score 256; DB 1; Length 205; Best Local Similarity 29.7%; Pred. No. 9.72e-27; Matches 38; Conservative 35; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                            TSUJIMOTO Y., CROCE C.M.;
PROC. NATL. ACAD. SCI. U.S.A. 83:5214-5218(1986)
                                                                                                01-WAR-1989 (REL. 10, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
PROTEIN BCL-2-BETA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (REL. 10, CREATED)
(REL. 25, LAST SEQUENCE UPDATE)
(REL. 32, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             239 AA
                                                       205 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EGUCHI Y., EWERT D.L., TSUJIMOTO Y.;
NUCLEIC ACIDS RES. 20:4187-4192(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                       PRT;
                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REVISIONS TO 96 AND 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION.
                                                                                                                                                                                                                                    SAPIENS (HUMAN).
                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE; 86259760.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             191 dnggwvga 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 92375724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 91066924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BC2A_HUMAN
P10415;
01-MAR-1989 (
01-APR-1993 (
01-NOV-1995 (
5
BC2B_HUMAN
P10416;
01-v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIM: 151430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 윱
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                                                       HDD DD BRAND DD BRAND BR
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MATCHEBERY D., NONEZ G., MILLIMAN C., SCHREIBER R.D., KORSMEYER S.J.;
NATURE 348:334-336(1990).
-!- FUNCTION: PROLOGES THE SURVIVAL OF HEMATOPOIETIC CELLS IN THE
ABSENCE OF REQUIRED GROWTH FACTORS AND ALSO IN THE PRESENCE OF
VARIOUS STIMULI INDUCING CELLULAR DEATH. BLOCKS APOPTOSIS. MIGHT
FUNCTION IN AN ANTIOXIDARY PACHWAY TO PREVENT APOPTOSIS. MIGHT
FUNCTION IN AN ANTIOXIDARY PACHWAY TO PREVENT APOPTOSIS AT SITES
OF FREE RADICAL GENERATION SUCH AS MITOCHONDRIA.
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE.
-!- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES.
-!- DISSEASE: INVOLVED IN FOLLICULAR LYMPHOMA (FL) (ALSO KNOWN AS TYPE
II CHRONIC LYMPHATIC LEGREMAIN BY A CHROMOSOMAL TRANSLOCATION
TICHAS (14.18) (Q32:Q21) WHICH INVOLVES BCLZ AND IMMUNOGLOBULIN GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   132 tvveelfrdgvnwgrivaffefggvmcvesvnremsplvdnialwmteylnrh-lhtwig 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74 tpaapgaaagpalspvppvvhlt--lrqagddfsrryrrdfaemssqlhltpftargrfa 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- ALTERNATIVE PRODUCTS: TWO FORMS OF BCL-2: ALPHA, AND BETA, AND PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THEY ONLY DIFFER AT THEIR C-TERMINAL ENDS.
-!- SINILARIY: BELONGS TO THE BCL-2 FAMILY.
EMBL, M13994; G17957; ALT_SEQ.
EMBL, M13994; G179371; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALTERNATIVE SPLICING; TRANSMEMBRANE;
                              HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 16.5%; Score 256; DB 1; Length 239; Local Similarity 29.3%; Pred. No. 9.72e-27; les 41; Conservative 37; Mismatches 57; Indels
                                                                                                                                                       PROC. NATL. ACAD. SCI. U.S.A. 83:5214-5218(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 59 P -> T (IN REF. 3).
117 117 S -> R (IN REF. 3).
239 AA; 26266 MW; 75084B59 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               199 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTO-ONCOGENE; APOPTOSIS; ALTERNATIVE SPI MITOCHONDRION; CHROMOSOMAL TRANSLOCATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                          MEDLINE; 92375724.
EGUCHI Y., EWERT D.L., TSUJIMOTO Y.;
NUCLEIC ACIDS RES. 20:4187-4192(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                            CLEARY M.L., SMITH S.D., SKLAR J.;
CELL 47:19-28(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       191 dnggwdafvel-ygpsmrpl 209
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                                                                                                                                                                                         REVISIONS TO 96; 110 AND 237
                                                                                                                                    ISUJIMOTO Y., CROCE C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PS01080; BCL2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A29409; TVHUAL.
PIR; A24428; TVHUBC.
PIR; C37332; C37332.
MIM; 151430; ---
PROSITE; PS01080; BCLZ
                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION. MEDLINE; 91066924.
PROTEIN BCL-2-ALPHA
                                                                                                  SEQUENCE FROM N.A. MEDLINE; 86259760.
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE; 87002488.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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Matches
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TISSUE-BRAIN;
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BCL2_RAT
P49950;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 9337574.

EGUCHI Y., EWERT D.L., TSUJIMOTO Y.;

EGUCHI Y., EWERT D.L., TSUJIMOTO Y.;

NUCLEIC ACIDS RES. 20:4187-4192[1992).

-1- FUNCTION: PROLONGS THE SURVIVAL OF HEMATOPOIETIC CELLS IN THE ABSENCE OF REQUIRED GROWTH FACTORS AND ALSO IN THE PRESENCE OF VARIOUS STIMULI INDUCING CELLULAR DEATH. BLOCKS APOPTOSIS. MIGHT FUNCTION IN AN ANTIOXIDARY TO PREVENT APPOPTOSIS AT SITES OF FREE RADICAL GENERALION SUCH AS MITOCHONDRIA.

-1- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE.

-1- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES.
                                                                                                                                                                                                                        1; Gaps
                                                                                                                                    EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALLA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=BALB/C; TISSUE-LIVER;
STRAIN=BALB/C; TISSUE-LIVER;
NEGELINE; 87187643.
CELL 49:455-463(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 251; DB 1; Length 199
Pred. No. 8.18e-26;
29; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            DIFFER AT THEIR C-TERMINAL ENDS.
-1-STMLLARITY: BELONGS TO THE BCL-2 FAMILY.
EMBL, M16506: G387110; -.
PIR; B25960; TVMSB1.
PROSTIE; PS01080; BCL2.
APOPTOSIS; ALTERNATYE SPLICING; MEMBRANE; MITOCHONDRION.
SEQUENCE 199 AA; 22299 MW; 3E60FA47 CRG32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          154 mcvesvnremsplvdnialwmteylnrh-lhtwiqdnggwvga 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-WAR-1989 (REL. 10, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-CCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
BCL2 OR BCL-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           236 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 16.2%;
Local Similarity 31.1%;
108 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                01-MAR-1989 (REL. 10,
01-MAR-1989 (REL. 10,
01-OCT-1996 (REL. 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REVISIONS TO 221-222.
                                                                        PROTEIN BCL-2-BETA.
BCL2 OR BCL-2.
MUS MUSCULUS (MOUSE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MUS MUSCULUS (MOUSE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EUTHERIA; RODENTIA.
                                                                                                                                                                                                              87187643
                                                                                                                                                                                            SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LT 8
BC2A_MOUSE
P10417;
                                                                                                                                                                                                                  MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94 lrragddfsrryrrdfaemssqlhltpftargrfatvveelfrdgvnwgrivaffefggv 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78 LAIIGDDINRRYDSEFQTMLQHLQPTAENAYEYFTKIASSLFESGINWGRVVALLGFSYR 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABSENCE OF REQUIRED GROWTH FACTORS AND ALSO IN THE PRESENCE OF VARIOUS STIMULI INDUCING CELLULAR DEATH, BLOCKS APOPTOSIS, MIGHT FUNCTION IN AN ANTIOXIDANT PATHWAY TO PREVENT APOPTOSIS AT SITES OF FREE RADICAL GENERATION SUCH AS MITOCHONDRIA.

-! SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE.

-! TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 targrfatvveelfrdgvnwgrivaffefggvmcvgsvnremsplvdnialwmteylnrh 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY).
-1- ALTERNATIVE PRODUCTS: TWO FORMS OF BCL-2: ALPHA, AND BETA, ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THEY ONLY DIFFER AT THEIR C-TERMINAL ENDS.
-i- ALTERNATIVE PRODUCTS: TWO FORMS OF BCL-2: ALPHA, AND BETA, ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THEY ONLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JENE 140:291-292(1994).
-1- FUNCTION: PROLONGS THE SURVIVAL OF HEMATOPOIETIC CELLS IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     154 mcvesvnremsplvdnialwmteylnrh-lhtwiqdnggwdafvel-ygpsmrpl 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                   -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
EMBL, 131523, G387109; --
EMBL, M16506; G387109; JOINED.
PIR; A25960; TVWASA.
PIR; B37332; E37332.
PROSITE; PSOLO180; BCL2.
APOPTOSIS; ALTERNATIVE SPLICING; TRANSMEMBRANE; MITOCHONDRION.
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ä
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EMBL. 114680; G408947; -.
APOPTOSIS; ALTERNATIVE SPLICING; TRANSMEMBRANE; MITOCHONDRION
TRANSMEM 209 230 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 16.1%; Score 250; DB 1; Length 236; Best Local Similarity 27.2%; Pred. No. 1.25e-25; Matches 40; Conservative 43; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                        Length 236
                                                                                                                                                                                                                                                                                                                                                                                                  Score 251; DB 1; Length 236
Pred. No. 8.18e-26;
31; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                            209 230 POTENTIAL.
236 AA; 26425 MW; 7ADFE975 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         230 POTENTIAL.
26550 MW; 336E6B40 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
BCL2 OR BCL-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              236 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SATO T., IRIE S., KRAJEWSKI S., REED J.C.;
GENE 140:291-292(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 -lhtwiqdnggwdafvel-ygpsmrpl 206
                                                               DIFFER AT THEIR C-TERMINAL ENDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1996 (REL. 34, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                  / Match
Local Similarity 30.4%;
nes 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 94193015.
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HOMO SAPIENS (HUMAN).
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MEDLINE; 93364978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LT 12
BAXB_HUMAN
Q07814;
                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 nmelgrmiadvdtdspre-vff-rvaadmfadgnfnwgrvvalfyfasklvlkalctkvp 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-CSTEL/6 X DBA/2 F1;
MEDILINE; 93364978.

MEDILINE; 93364978.

CELL 74:609-619(1993).

-1- FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO THE APOPTOSIS REPRESSOR BCL 2.

-1- ALTERNATIVE PRODUCTS: A 21 KD MEMBRANE PROTEIN ALPHA AND THE TWO CYTOPLASMIC PROTEINS BETA AND GAMMA ARE GENERATED BY ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 seqimktgafllqgfiqdragrmagetpeltleqppqdastk-klsec1rrigdelds-- 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- SUBCELLUIAR LOCATION: MEMBRANE.
-1- SUBCELLUIAR LOCATION: MEMBRANE.
-1- SUBLERIV: BELDINGS TO THE BCL-2 FAMILY.
-2472, G388192.
- PROSITE; PSO1080; BCL2.
- PROSITE; PSO1081; BCL2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO THE APOPTOSIS REPRESSOR BGL-2.
SUBUNT: FORMS HOWOLMERS AND HETERODIMERS TOGETHER WITH BCL-2.
SUBCELLULAR LOCATION: MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
                                                                                                                                                                                                                                                                MUS MUSCULUS (MOUSE).
EUKARYOTA; META2OA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 14.2%; Score 221; DB 1; Length 192; Local Similarity 25.6%; Pred. No. 2.37e-20; les 46; Conservative 50; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
APOPTOSIS REGULATOR BAX, MEMBRANE ISOFORM ALPHA.
                                                                                                                                               01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-07-1996 (REL. 34, LAST ANNOTATION UPDATE)
APOPTOSIS REGULATOR BAX, MEMBRANE ISOFORM ALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BD035304 CRC32;
                                                                                                              192 AA.
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OLTVAI Z.N., MILLIMAN C.L., KORSMEYER S.J.;
CELL 74:609-619(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             192
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166 CIARWIAQRGGWVAALNLGNGPILNVL 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                            PRT;
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                                                                                                            STANDARD;
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                                                                                  LT 10
BAXA_MOUSE
Q07813;
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Q07812;
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47 OEAEGAAAPADPEMVTLPLQPSSTMGQVGRQLAIIGDDINRRYDSEFQTMLQHLQPTAEN 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          32 qdragrmggeapelaldpvpqdastkklseclkrigdelds--nmelgrmiaavdtdspr 89
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CELL 74:609-619(1993).
-!- FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO THE
APOPTOSIS REPRESSOR BCL-2.
-!- SUBGUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2.
-!- SUBCELLOUAR LOCATION: CYTOPLASMIC.
-!- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE
CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY
ALTERNATIVE SPLICING.
-!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
EMBL; L22474; G388168; -.
PIR; B47538; B47538.
-!- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELL'A ARE GENERATED BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
9
                                                                                                                                                                                                                                                                                                                                              Length 192;
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Pred. No. 3.69e-17;
36; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                        Match 13.4%; Score 208; DB 1; Length 192 Local Similarity 24.5%; Pred. No. 4.87e-18; les 40; Conservative 45; Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            147 rllgwiqdqggwdgllsyfgtptwqtvtifvagvltasltiwk 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   166 CIARWIAQRGGWVAALNIGNGPI-LNVLVVVLGVVLLGQFVVRR 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
APOPTOSIS REGULATOR BAX, CYTOPLASMIC ISOFORM BETA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MIM; buduyav,
PROSITE; PS01080; BCL2.
APOPTOSIE; ALTERNATIVE SPLICING.
                                                                                                                                                                                          PROSITE; PSÓ1080; BCL2.
APOPTOSIS; TRANSMEMBRANE; ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                      172 192 POTENTIAL.
192 AA; 21184 MW; B2E6148A CRC32;
                                             ALTERNATIVE SPLICTNG.
-!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY EMBL: L22473; G388166; -.
PIR; A47538; A47538.
MIM; 600040; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ą
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Best Local Similarity 27.0%;
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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TRANSMEM
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Gaps
                                                                                                                                                                                                                                                                                                                                                       APECINE; 9531797.

APTE S.S., MATTEI M.-G., OLSEN B.R.;
APTE S.S., MATTEI M.-G., OLSEN B.R.;
CENOMICS 26:592-594(1995).

-!- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY ALTERNATIVE SPLICING.

-!- SUBCELLUIAR LOCATION: CYTOPLASMIC (POTENTIAL).

-!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.

EMBL: JUSSEY; G841238; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KOZOPAS, K.M., YANG T., BUCHAN H.L., ZHOU P., CRAIG R.W.;
PROC. NATL. ACAD. SCI. U.S.A. 90:3516-3520(1993).
-!- FUNCTION: INVOLVED IN PROGRAMMING OF DIFFERENTIATION AND CONCOMITANT MAINTENANCE OF VIABILLITY BUT NOT OF PROLIFERATION
                                                                                                                                                                                                                                                                        HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HOMO SAPIENS (HUMAN).
EUKARYOTA; METALOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
INDUCED MYELOID LEUKEMIA CELL DIFFERENTIATION PROTEIN MCL1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 178; DB 1; Length 143;
Pred. No. 7.38e-13;
31; Mismatches 43; Indels
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163 LHHCIARWIAQRGGWVAALNLGNPI-LNVLVVLGVVLLGGPVVRR 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APOPTOSIS; ALTERNATIVE SPLICING.
SEQUENCE 143 AA; 15772 MW; 71AA1CBD CRC32;
                                                                                                   350 AA
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APOPTOSIS; TRANSMEMBRANE; DIFFERENTIATION.
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TISSUE-MYELOID LEUKEMIA CELLS;
MEDLINE; 93234528.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 27.4%;
Matches 29; Conservative
                                       166 CIARWIAQRGGWVALN 182
147 rllgwigdgggwyrllk 163
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Q07820;
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-!- INDUCTION: BY GRAULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR AND LPS IN MACROPHAGES.
-!- SUBCELLULAR LOCATION: INTRACELLULAR.
-!- TISSUE SPECIFICITY: EXPRESSED IN HEMOPOIETIC TISSUES, INCLUDING BONE MARROW, SPLEEN AND THYMUS.
-!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
EMBL; L16462; Q293274; --
PROSITE: PS01080; BCL2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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J. IMMUNOL. 151:1979-1988(1993).
-!- FUNCTION: MAY FUNCTION IN THE RESPONSE OF HEMOPOIETIC CELLS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88 rivtifafggvllkklpqeqialdvcaykqvssfvaefimnn-tgewirqnggw 140
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALLA;
EUTHERIA; RODENTIA.
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                                                                                                             Length 350;
                                                                                                     Score 179; DB 6; Length 350
Pred. No. 5.01e-13;
29; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
HEMOPOIETIC-SPECIFIC EARLY RESPONSE PROTEIN (A1 PROTEIN)
                                                                                                                                                                                                                                                                                                                   273 fvakhlktingescieplaesitd-vlvrtkrdwlvkgrgw 312
                                                                                                                                                                                                                                                                                                                                                                       137 RLALHIYQRGLTGFLGQVTRFVVDFMLHHCIARWIAQRGGW 177
227 227 OR A.
330 349 POTENTIAL.
350 AA; 37365 MW; 10194B64 CRC32;
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SEQUENCE 172 AA; 19914 MW; FFD38D6F CRC32;
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STRAIN-CBA/J; TISSUE-BONE MARROW;
MEDLINE; 93346743.
                                                                                                     Query Match
Best Local Similarity 25.7%;
Matches 26; Conservative
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HSAL_MOUSE
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Wed Aug 20 11:05:33 1997; MasPar time 8.89 Seconds 685.993 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-320-157-9 (1-211) from USO8320157.pep 1554 1 MASGGPGPPRQECGEPALP......LVVLGVVLLGQFVVRRFFKS 211 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

91006 seqs, 28888923 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

pir51 Database:

1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3 8:unann4 9:unann5 10:unann6 11:unann7 12:unann8 13:unann9 14:unann10 15:unenc 16:unrev

Mean 45.185; Variance 108.828; scale 0.415 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Pred. No.	1.43e-241	3.45e-237	1.24e - 23	5.03e-23	3.55e-23	3.55e-23	7.14e-23	1.43e-22	4.08e-22	5.77e-22	2.31e-21	2.31e-21	1.30e-20	1.30e-20	1.30e-20	1.30e-20	2.60e-20	5.72e-19	5.02e-16	2.74e-14	1,43e-13
		Description	cdn-2 protein - huma	Bak protein - human	apoptosis requlator	transforming protein	BCL-X protein - rat	bcl-x long - mouse	transforming protein	apoptosis requlator	bcl-x transmembrane	transforming protein			transforming protein	BCL-X-Long - rat	transforming protein	transforming protein	BCL-2 - rat (fragmen	transforming protein	programmed cell deat	bcl-2-associated pro	bcl-2-associated pro
SUMMARIES	£	TD	S58875	S58873	A47537	B37332	S51761	I49056	A37332	B47537	149057	TVHUB1	D37332	TVHUA1	TVMSB1	I67431	TVMSA1	E37332	167432	S24390	D47538	A47538	B47538
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RESULT

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187 182 178 173 117 117 107 107 105 105 103	100 100 100 100 98 97
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## ALIGNMENTS

\$58875 #type complete cdn-2 protein - human #formal_name Homo sapiens #common_name man 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 558875 \$58874	s	ab 116 0t m	larity 100.0%; Pred. No. 1.43e-241; Conservative 0; Mismatches 0; pprqecgepalpsaseeqvaqdteevfrsyvfyhhq	vtlplqpsstmgqvgrqlaiigddinrrydsefqtmlqhlqptaenayeyftkiasslfe 120 	sginwgrvvallgfsyrlalhiygrgltgflggvtrfvvdfmlhhciarwiagrggwvaa 180 	lnigngpilnvlvvlgvvllggfvvrrffks 211 
RESULT 1 ENTRY TITLE ORGANISM DATE ACCESSIONS REFERENCE	#authors #journal #title #accession #*status	##residues ##cross-re ##note SUMMARY Query Match	Best Local Simi: Matches 211; I masgggpour   1 masg	61 vt    61 VT	121 sg 	181 ln 
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                                                                                                                                                                                                                                                                                                                                                                           Kiefer, M.C.; Brauer, M.J.; Powers, V.C.; Wu, J.J.; Umansky, S.R.; Tomei, L.D.; Barr, P.J.
Nature (1995) 374:736-739
Modulation of apoptosis by the widely distributed Bcl-2
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S58873 *type complete
Bak protein - human
bol-2 homolog; complete
fformal_name Homo sapiens *common_name man
15.Feb-1996 *sequence_revision 01-Mar-1996 *text_change
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:Y #length 211 #molecular-weight 23409 #checksum 801
                                                                                      S58873
Chittenden, T.; Harrington, E.A.; O'Connor, R.; Fl.
C.; Lutz, R.J.; Evan, G.I.; Guild, B.C.
Nature (1995) 374:733-736
Induction of apoptosis by the Bcl-2 homologue Bak.
                                                                                                                                                     ***status preliminary; nucleic acid sequence not shown ##molocule_type mRNA
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Nucleic Acids Res. (1992) 20:4187-4192
Isolation and characterization of the chicken bcl-2 gene:
expression in a variety of tissues including lymphoid and
neuronal organs in adult and embryo.
Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.;
Lindsten, T.; Turka, L.A.; Mao, X.; Nunez, G.; Thompson,
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BCL-X protein - rat
*formal_name Rattus norvegicus *common_name Norway rat
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FICATION #superfamily bcl transforming protein
Y #length 216 #molecular-weight 23492 #checksum 3596
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17.2%; Score 267; DB 6; Length 216;
Best Local Similarity 28.5%; Pred. No. 5.03e-23;
Matches 39; Conservative 39; Mismatches 55; Indels
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                                                                                                                                                                                          ##status preliminary
##molecule_type DNA
##residues 1-190 ##label BOI
##cross-references GB:L20120

XY #length 190 #molecular-weight 21467
                                                                                                                                                                                                                                                                                                                                                                   Query Match 17.4%; Score 271; DB 13; L. Best Local Similarity 28.1%; Pred. No. 1.24e-23; Matches 34; Conservative 36; Mismatches 49;
                                                                           cell (1993) 74:597-608
bcl-x, a bcl-2-related gene that fur
regulator of apoptotic cell death.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #authors Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.
#journal J. Immunol. (1994) 155:4388-4398
#title Cloning and molecular characterization of mouse bcl-x in and T lymphocytes.
#cross-references MUID:95052604
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submitted to the EMBL Data Library, November 1994
IL-5 inhibits anti-IgM-induced apoptosis in an immature
cell line through inductin of bcl-X1.
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#formal_name Mus musculus #common_name house mouse
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
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#length 233 #molecular-weight 26130 #checksum 6378
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##residues 1-233 ##label RES
##cross-references EMBL:U10101; NID:9506647; CDS_PID:9506648
NACE S52866
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Michaelidis, T.M.
submitted to the EMBL Data Library, November 1994
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Michaelidis, T.M.
submitted to the EMBL Data Library, November 1994
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Pred. No. 3.55e-23;
37; Mismatches 46; Indels
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Pred. No. 3.55e-23;
37; Mismatches 46; Indels
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##cross-references EMBL:X83574
Y #length 233 #molecular-weight 26132
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##cross-references EMBL:X82537
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Best Local Similarity 28.0%;
Matches 33; Conservative
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Best Local Similarity 28.0%;
Matches 33; Conservative
               01-Dec-1995
S51761; S51762
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##residues 1-2
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Lindsten, T.; Turka, L.A.; Mao, X.; Nunez, G.; Thompson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 hhrpeppgsaaasevppae-glrpapp-g-vhlalrqagdefsrrygrdfaqmsgqlhlt 116
                                                                                                                                                                                                                                                           Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. (1992) 20:4187-4192
Isolation and characterization of the chicken bcl-2 gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44 QQEQEAEGAAAPADPEMVTLPLQPSSTMGQVGRQLAIIGDDINRRXDSEFQTMLQHLQPT 103
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Cell (1993) 74:597-608
bcl-x, a bcl-2-related gene that functions as a dominant regulator of apoptotic cell death.
B47537
                                                                                              transforming protein (bcl-2-alpha) - chicken
transforming protein (bcl-2-alpha) - chicken
#formal_name_Gallus gallus #common_name chicken
03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change
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143 ffsfggalcvesvdkemqvlvsriaswmatylndh-lepwiqenggwdtfvdlygnna
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Pred. No. 7.14e-23;
42; Mismatches 56; Indels
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apoptosis regulator bcl-xs
#formal_name Homo sapiens #common_name man
16-Aug-1996 #sequence_revision 16-Aug-1996
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transforming protein
#length 233 #molecular-weight 25687
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apoptosis regulator bcl-xL - human
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##cross-references GB:L20121; CDS_PID:Q07817
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#cross-references MUID:86259760
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Proc. Natl. Acad. Sci. U.S.A. (1986) 83:5214-5218
Analysis of the structure, transcripts, and protein products
of bci-2, the gene involved in human follicular lymphoma.
                                                                                                                             *label MAT\
*product apoptosis regulator bcl-xS *status predicted
                                                                                                               *product apoptosis regulator bcl-xL *status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #authors Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.
#Journal J. Immunol. (1994) 153:4388-4398
#title Cloning and molecular characterization of mouse bcl-x in and T lymphosytes.
#cross-references MUID:95052604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYHUB] *type complete transforming protein bcl-2-beta - human *formal_name Homo sapiens *common_name man 31-bec-1988 *sequence_revision 31-bec-1988 *text_change 06-sep-1996
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                                                                                                                                                                                                                                                                                                                                       143 ffsfggalcvesvdkemqvlvsriaawmatylndh-lepwiqenggwdtfvelygnna 199
                                                                                                                                                                                                                                                                                                                                                            #length 233 #molecular-weight 26063 #checksum 5340
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#length 214 #molecular-weight 23900 #checksum 9730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 261; DB 14; Length 214;
Pred. No. 4.08e-22;
33; Mismatches 43; Indels
                                                                                                                                                                                                               Length 233;
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                                                                                                                                                                                                                                             37; Mismatches 46; Indels
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##cross-references GB:L20122; CDS_PID:g623237
                                                                                                                                                                                                                                                                                                                                                                                                                                      149057 #type complete
bcl-x transmembrane deleted - mouse
                                                                                                                                                                                                           Score 264; DB 13;
Pred. No. 1.43e-22;
                                             ##cross-references GDB:228079
alternative splicing; apoptosis
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                                                                                                                                                                                                           17.0%; :larity 28.0%; | Conservative
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Best Local Similarity 28.0%;
Matches 30; Conservative
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#Gene GDB:BCL2
##cross-references GDB:119031
#map_position 18041.33-180421.33
CLASSIFICATION #superfamily bol transforming protein
Alternative splicing; B-cell lymphoma; follicular lymphoma;
transforming protein
#Index 
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Nucleic Acids Res. (1992) 20:4187-4192
Isolation and characterization of the chicken bcl-2 gene:
expression in a variety of tissues including lymphoid and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 tvveelfrdgvnwgrivaffefggvmcvesvnremsplvdnialwmteylnrh-lhtwiq 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75 tpaapgaaagpalspvppvvhlt--lrqagddfsrryrrdfaemssglhltpftargrfa 132
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*length 206 *molecular-weight 22440 *checksum 5581
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Pred. No. 2.31e-21;
35; Mismatches 51;
*crossion BZy*v,
*accession BZy*v,
**molecule_type mRNA
**molecule_type mRNA
1-205 **label TSU
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Best Local Similarity 29.7%;
Matches 38; Conservative
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Best Local Similarity 29.7%;
Matches 38; Conservative
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#journal Proc. Natl. Acad. Sci. U.S.A. (1986) 83:5214-5218
#title Analysis of the structure, transcripts, and protein products of bol.2, the gene involved in human follicular lymphoma.
#cross-references MuID:86259760
#accession A29409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #authors Seto, M.; Jaeger, U.; Hockett, R.D.; Graninger, W.; Bennett, S.; Goldman, P.; Korsmeyer, S.J.
#journal ExBo J. (1988) 7:123-131
#title Alternative promoters and exons, somatic mutation and deregulation of the Bcl-2--Ig fusion gene in lymphoma.
#cross-references MUID:88196071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #authors Hua, C.; Zorn, S.; Jensen, J.P.; Coupland, R.W.; Ko, H.S.; Wright, J.J.; Bakhshi, A.
#journal Oncogene Res. (1988) 2:263-275
#title Consequences of the t(14;18) chromosomal translocation in follicular lymphoma: deregulated expression of a chimeric and mutated BCL-2 gene.
                                                         Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. (1992) 20:4187-4192
Siolation and characterization of the chicken bcl-2 gene:
expression in a variety of tissues including lymphoid and
neuronal organs in adult and embryo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 1-95,'A',97-109,'G',111-236,'S',238-239 ##label TSU
this sequence has been corrected in reference A37332
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                                                                                                                                                                              nucleic acid sequence not shown; not compared with conceptual translation
                   C37332; A29409; S02452; A24428; A27622; B27622
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##residues 1-58,'T',60-116,'R',118-239 ##label CLE
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this report is a correction
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##residues 1-58,'T',60-239 ##label HUA
cession B27622
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##residues 1-239 ##label SET
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#map_position 18q21.33-18q21.33
06-Sep-1996
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##molecule_type mRNA
##residues 1-95,
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##residues 1-6,
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##residues 1-23
##note this
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMMENT
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Cell (1987) 49.455-463
Molecular analysis of mbcl-2: structure and expression of the
murine gene homologous to the human gene involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L. Endocrinology (1995) 136:232-241
Expression of members of the bcl-2 gene family in the immature rat ovary: equine chorionic gonadotropin-mediated inhibition of granulosa cell apoptosis is associated with decreased bax and constitutive bcl-2 and bcl-xlong messenger ribonucleic acid levels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ä
                                                                                                                                                                                                                       74 tpaapgaaagpalspvppvvhlt--lrqagddfsrryrrdfaemssqlhltpftargrfa 131
                                                                                                                    132 tvveelfrdgvnwgrivaffefggvmcvesvnremsplvdnialwmteylnrh-lhtwig 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78 LAIIGDDINRRYDSEFQTMLQHLQPTAENAYEYFTKIASSLFESGINWGRVVALLGFSYR 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Negrini, M.; Silini, E.; Kozak, C.; Tsujimoto, Y.; Croce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transforming protein bol-2-beta - mouse
#formal_name Mus musculus #common_name house mouse
31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           167431 #type complete
BCL-X-Long - rat
#formal_name Rattus norvegicus #common_name Norway rat
26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
26-Jul-1996
167431
153295
                                   Gaps
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alternative splicing; transforming protein
#length 199 #molecular-weight 22299 #checksum 7397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 251; DB 2; Length 199;
Pred. No. 1.30e-20;
29; Mismatches 41; Indels
                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 29.3%; Pred. No. 2.31e-21; Matches 41; Conservative 37; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #type complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1-199 ##label NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   follicular lymphomā.
#cross-references MUID:87187643
                                                                                                                                                                                                                                                                                                                                   : ||| | ::| || : |
173 QRGGWVAALNLGNGPILNVL 192
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                                                                                                                                                                                                                                                                                                   191 dnggwdafvel-ygpsmrpl 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 16.2%;
Best Local Similarity 31.1%;
Matches 32; Conservative
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##residues 1-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##molecule_type DNA
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                                                                                                           83 maavkqalreagdefelryrrafsdltsqlhitpgtvyqsfeqvvnelfrdgvnwgriva 142
                                                                                                                               94 lrragddfsrryrrdfaemssqlhltpftargrfatvveelfrdgvnwgrivaffefggv 153
                                                                                                                                                                                                                                                                          2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                     #journal Cell (1987) 49:455-463
#title Molecular analysis of mbcl-2: structure and expression murine gene homologous to the human gene involved in follicular lymphoma.
#cross-references MUID:87187643
#accession A25960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Gaps
                                                                                                                                                                          BCL2
192/3
#superfamily bcl transforming protein
#superfamily bcl transforming protein
#length 236 #molecular-weight 26524 #checksum 6709
##cross-references EMBL:034963; NID:91004376; CDS_PID:91004377 (Y #length 233 #molecular-weight 26122 #checksum 8310
                                             Score 251; DB 14; Length 233;
Pred. No. 1.30e-20;
34; Mismatches 48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 16.2%; Score 251; DB 2; Length 236; Best Local Similarity 30.4%; Pred. No. 1.30e-20; Matches 35; Conservative 31; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##molecule_type DNA
##residues 1-236 ##label NEG
                                             Query Match
Bost Local Similarity 27.6%;
Matches 32; Conservative
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CLASSIFICATION
KEYWORDS
SUMMARY
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REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                          #authors
                                                                                                                                                                                                                                                                                          TITLE
ORGANISM
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Search completed: Wed Aug 20 11:05:58 1997 Job time : 25 secs.

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Wed Aug 20 11:08:18 1997; MasPar time 3.38 Seconds 298.086 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-320-157-21 (1-88) from US08320157.pep 643 Title: Description: Perfect Score: Sequence:

88

1 MASGOGPGPPRQECGKPALP.....APWGRWDGSSPSPGRHQPAL

PAM 150 Gap 11 Scoring table:

96640 seqs, 11439865 residues Searched:

Post-processing:

Minimum Match 0% Listing first 45 summaries

Database:

i.part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 a-geneseq27

Mean 27.717; Variance 105.074; scale 0.264 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

NO.	-58	-12	-12	-12	1-12	-12	00+	13e+00	+01	34e+01	34e+01	34e+01	62e+01	62e+01	+01	+01	36e+01	+01	+01	+01
Pred.	1.98e-5	3.66e-	3.66e-	3.66e-	3.66e-	3.66e-1	7.53e+0	9.136	1.11e+0	1.346	1.346	1.346	1.62€	1.62€	1.62e+0	1.95e+0	2.36e	2.36e+0	3.43e+0	3.43e+01
Description	Human Cdn-3.	Bak-2 protein.	Human Cdn-1.	Bak protein.	Bcl-Y apoptosis-relat	Human Cdn-2.	Xenopus laevis HSP (x	Mature mouse sperm 70	Gallus gallus HSP (ch	Human interleukin-I-c	Aromatic dihydrodiol/	Human neuronal calciu	HSV L/ST ORF1.	Murine Natural Killer	Partial Human Natural	Mouse SLIP1 homologue	MN protein.	Rat HSP (rathsp70).	Human alpha-1A adrene	Human alpha-1A adrene
GI GI	R77878	W03669	R77876	W03668	R81451	R77877	R03928	R43004	R03930	R95830	R66729	R71007	R64327	R13320	R13319	R43002	R41746	R03927	R70996	R90040
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Score	643	213	213	213	213	213	84	83	82	81	81	81	80	80	80	79	78	78	92	16
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Insulinoma-associated erya region polypepti Phytase protein.  BRCA1 mutant from pat BRCA1 allele #77 tran BRCA1 allele #8403 tr BRCA1 mutant from PM2 BRCA1 mutant from PM2 BRCA1 mutant from PM2 BRCA1 mutant from PM0 BRCA1 mutant from Sam BRCA1 mutant from pat
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### ALIGNMENTS

New nucleic acid sequences encoding Cdn apoptosis modulators - and related vectors, transformed cells, proteins and antibodies, useful or diagnosis and treatment e.g. of HIV infection, reperfusion injury cdn-3; apoptosis modulator; adoptive immunotherapy; therapy; HIV; autoimmune disease; reperfusion injury; hepatitis, osteoporosis; shock; lymphoma; eczema. Disclosure; Fig.7B-C; 66pp; English.
Southern blot analysis of human genomic DNA and a panel of human/rodent somatic cell DNAs revealed at least 3 Cdn-related genes residing on chromosomes 6, 11 and 20. Cdn-3 (R77878) did not contain the structural features of Cdn-1 (R77876), Cdn-2 Sequence 88 AA; Length 88; .r 1 R77878 standard; Protein; 88 AA. 08-JUN-1994; U.13930. 30-NOV-1994; U.13930. 30-NOV-1994; US-160067. 07-OCT-1994; US-320157. (LXRB-) LXR BIOTECHNOLOGY INC. BAIT PJ. KIEGER MC; WPI: 95-215106/28. 21-NOV-1995 (first entry) Homo sapiens. W09515084-A. Human Cdn-3 RESULT RE

1 masgggppprgecgkpalpsaseeqvaqdmegfsaatffttisrnrrlkgrpplptgrw 60 Gaps ; 0 Score 643; DB 13; Length 88 Pred. No. 1.98e-58; 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.0%;
Matches 88; Conservative g

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SPCPSNLAAPWGRWDGSSPSPGRHQPAL 88 61 spcpsnlaapwgrwdgsspspgrhgpal 88

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(IMMU-) IMMUNOGEN INC
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                    Query Match
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                                                                                                                                                                                                                                                                                       This Bak-2 protein sequence represents a bc1-1 homologue which interacts with Epstein-Barr virus (EBV) early lytic cycle BHRF1 protein, and is capable of modulating apoptosis. The protein may be used in complete or partial form, or as an epitope tag fusion protein, in a new virucide drug screening method, which involves combination of Bak-2 protein and a viral protein (e.g. EBV BHRF1), exposure to a test compound, and monitoring for disruption of the interaction, e.g. by co-precipitation, protein interactive trapping or ELISA. Interaction of Bak-2 and viral proteins allows viral replication or latency in the absence of apoptosis. Compounds which inhibit the interaction may be used as virucide, antitumour or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; 095492.
New nucleic acid sequences encoding Cdn apoptosis modulators - and related vectors, transformed cells, proteins and antibodies, useful or diagnosis and treatment e.g. of HIV infection, reperfusion injury
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig. 3A-B; 66pp; English.

Cdn-1 cDNA was isolated from a human heart cDNA library using a Cdn-1 cDNA was isolated from a human heart cDNA library using a proviously isolated clone as probe. Recombinant Cdn-1 was produced in Sf9 and human colon adenocarcinoma HT29 calls. Expression of Cdn-1 in WI-L2 lymphoblastoid cells resulted in increased cell survival in response to anti-Fas-mediated apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV; autoimmune disease; reperfusion injury; hepatitis, osteoporosis; shock; lymphoma; eczema.
                                                      Human; Bak-2; apoptosis; latency; virus replication;
Eperein-Barr Virus; BHRF1; fusion protein; epitope tag;
drug screening; co-precipitation; ELISA; immunoassay; antibody;
protein interactive trapping; virucide; antitumour; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                     Screening for anti-viral agents - by detecting the ability of agent to disrupt the interaction of a Bak protein and a viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         n 33.1%; Score 213; DB 20; Length 211; Similarity 78.0%; Pred. No. 3.66e-12; 32; Conservative 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MASGGFGPPRQECGKPALPSASEEQVAQDMEG-FSAATFF 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 masgqqppprqecqepalpsaseeqvaqdteevfrsyvfy 41
W03669 standard; Protein; 211 AA. W03669;
                                                                                                                                                                                                                                                                   protein
Disclosure; Fig 2; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R77876 standard; Protein; 211 AA.
                                                                                                                                      24-OCT-1996.
19-APR-1996.
20-APR-1995; US-426529.
(LXRB-) LXR BIOTECHNOLOGY INC.
BART PJ. Klafer MC;
WPI; 96-485886/48.
N-PSDB; T42139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-JUN-1995.
30-NOV-1994; U13930.
30-NOV-1994; US-160067.
07-OCT-1994; US-320157.
(LXRB-) LXR BLOTECHNOLOGY INC.
Barr PJ. Klafer MC;
WPI; 95-215106/28.
                           22-FEB-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-NOV-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnostic agents.
Sequence 211 AA;
                                         Bak-2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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This Bak protein sequence represents a bcl-1 homologue which interacts with Epstein-Barr virus (EBV) early lytic cycle BHRR1 protein, and is capable of modulating apoptosis. The protein may be used in complete or partial form, or as an epitope tag fusion or protein, in a new virucide drug screening method, which involves combination of Bak protein and a viral protein (e.g. EBV BHRR1), exposure to a test compound, and monitoring for disruption of the interaction, e.g. by co-precipitation, protein interactive trapping or ELISA. Interaction of Bak and viral proteins allows viral replication or latency in the absence of apoptosis. Compounds which inhibit the interaction may be used as virucide, antitumour or diagnostic agents.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                        Human; Bak; apoptosis; latency; virus replication; Epstein-Barr virus; BHRF1; fusion protein; epitope tag; drug screening; co-precipitation; ELISA; immunoassay; antibody; protein interactive trapping; virucide; antitumour; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ij
                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Screening for anti-viral agents - by detecting the ability of agent to disrupt the interaction of a Bak protein and a viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BCl-Y apoptosis-related protein.
BCl-Y; apoptosis; cell proliferation; cell death; diagnosis;
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  Length 211;
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Pred. No. 3.66e-12;
2; Mismatches 6; Indels
                                                       Indels
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9
                                                                                                           1 masgqqppprqecgepalpsaseeqvaqdteevfrsyvfy 41
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/note- "putative membrane localisation sequence"
WO9605232-A1.
Score 213; DB 13;
Pred. No. 3.66e-12;
                                                       2; Mismatches
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                                                                                                                                                                                                                                                                               standard; Protein; 211 AA
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20-APR-1995; US-426529.
(LXRB-) LXR BIOTECHNOLOGY INC.
Balt PJ, Klefer MC;
WPI; 96-485886/48.
33.1%;
78.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 33.1%;
Best Local Similarity 78.0%;
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                   22-FEB-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-JUL-1996 (first entry)
                          Best Local Similarity 78.0%;
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-FEB-1996.
09-AUG-1995; U10103.
09-AUG-1994; US-287427.
11-OCT-1994; US-321071.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; T42138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9633416-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo saptens.
                                                                                                                                                                                                                                                                                                                                                                   Bak protein.
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Query Match
      셤
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                                                                                                 or cell death

Claim 3: Fig 4: 100pp; English.
Claim 5: Fig 4: 100pp; English.
Claim 5: Fig 4: 100pp; English.
Claim 6: Fig 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ij
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                                                            New isolated human Bcl-Y protein - used to develop prods. for treating disorders characterised by inappropriate cell proliferation or cell death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; Q95493.
New nucleic acid sequences encoding Cdn apoptosis modulators - and related vectors, transformed cells, proteins and antibodies, useful or diagnosis and treatment e.g. of HIV infection, reperfusion injury
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cdn-2; apoptosis modulator; adoptive immunotherapy; therapy; HIV
autoimmune disease; reperfusion injury; hepatitis, osteoporosis;
shock; lymphoma; eczema.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        etc.
Disclosure; Fig.5D-E; 66pp; English.
Cdn-2 cDNA was isold. from a human placental genomic library
cdn-2 cDNA was isold. from a human placental genomic library
using a 950 bp fragment of Cdn-1 cDNA. Expression of Cdn-2
in mouse progenitor B-cell FL5.12 cells decreased IL-3-induced
appropria: The Cdn-2 protein displayed 97% amino acid identity
with Cdn-1 (R77876).
Sequence 211 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ÷
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R03928;
30-40G-1990 (first entry)
Kenopus laevis HSP (x170).
HSp70; heat shock protein; Trypanosoma cruz1; vaccines; HSP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 masgqgpgpprqecgepalpsaseeqvaqdteevfrsyvfy 41
                                                                                                                                                                                                                                                                                                                                                                                                    Score 213; DB 17;
Pred. No. 3.66e-12;
2; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 213; DB 13;
Pred. No. 3.66e-12;
2; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ä
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30-NOV-1993; US-160067.
07-OCT-1994; US-320157.
(LARB-) LAR BIOTECHNOLOGY INC.
BARY PJ, KLOFER MC;
WPI; 95-215106/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T
R77877 standard; Protein; 211
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 33.1%;
Best Local Similarity 78.0%;
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 33.1%;
Best Local Similarity 78.0%;
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                    WPI; 96-139648/14.
N-PSDB; T17375.
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WO9515084-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R77877;
21-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-JUN-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human Cdn-2
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ID RO
AC RO
DT 30
DE XE
KW HE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11. Serratia marcescens (smahsp70 - R03932).
The proteins having homology to hsp's of T. cruzi can be used in avecines and diagnosis involving e.g. Trypanosoma, Mycoplasma and Mycobacteria species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-MXY-1994 (first entry)
Adture mouse sperm 70kD heat shock protein.
Sulphoglycolipid immobilising protein 1; sperm plasma membrane;
HSC70B; mammalian; infertility; mycoplasma; HSP70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ä
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Pred. No. 7.53e+00;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           265 rtacdrakrtlssssqasieidslfegidfytaitrar 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8

R43004 standard; protein; 641 AA.

DE R43004

T 20-MAY-1994 (first entry)

DE Mature mouse sperm 70kD heat shock p

KW Sulphoglycolipid immobilising protein

KW MISC70B; mammalian; infertility; mycc

Mus musculus.

L.385

FT Region

FT /label= 44kD_ATPase_fragment

FT /note= "peptides comprising an intac

FT /note="peptides are homologous to seque

FT mycoplasme protein."

FT /note= "part"

FT /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.1%;
26.3%;
12-SEP-1989; 03955.
12-SEP-1988; US-243474.
(CODO-) Codon.
Dragon E, Faulds D, Sias S.
WPI: 90-115820/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 26.3%;
Matches 10; Conservative
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Sequence Query Match

Matches

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Human interleukin-I-converting enzyme-like apoptosis protease-3. 
ICE-LAP-3; interleukin-I-converting enzyme-like apoptosis protease; enzyme; Alzheimer's disease; Parkinson's disease; septic shock; head injury; rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Numan ICE-LAP-3 and -4 DNA and protein - useful in the diagnosis and treatment of Alzheimer's disease, Parkinson's disease, rheumatoid arthritis, septic shock and head injury (Laim i, Page 91-92; 67pp; English.

This ICE-LAP-3 protein may be used therapeutically, e.g. as an antitumor or antiviral agent and to control embryonic development and tissue homeostasis. The protein can also be used to treat immunosuppression disorders, such as AIDS, by targeting virus infected cells for cell death. The DNA may find use in gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 12.6%; Score 81; DB 18; Length 341 Best Local Similarity 40.0%; Pred. No. 1.34e+01; Matches 12; Conservative 8; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49 lkgpqtlaaerrretvpvpaalp-pwerwq 77
                                                                     R95830 standard; Protein; 341 AA. R95830;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T 11
R66729 standard; Protein; 459 AA.
                                                                                                                                                                                                                                                                                                                                                                                           06-JUN-1995; U07235.
01-NOV-1994; US-334251.
(HUMA-) HUMAN GENOME SCI INC.
Hastings GA. He W. Hudson PL,
WPI; 96-23959/24.
N-PSDB; T15276.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.6%;
ilarity 30.0%;
Conservative
                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-DEC-1994.
10-JUN-1993; 165163.
10-JUN-1993; JP-165163.
(SHOW ) SHOWA DENKO KK.
WPI; 95-069306/10.
N-PSDB; Q79907.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                        28-OCT-1996
                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                       09-MAY-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J06343474-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proteins homologues to heat shock proteins from Trypanosoma cruzi - used in vaccines and diagnosis for species of eg Mycoplasma or Mycobacteria. Disclosure; Fig 2.1-2.14; 86pp; English.

According to the lagend of Fig 2. the G. gallus HSP sequence has according to the lagend of Fig 2. the G. gallus HSP sequence has including "O" (?) at position 634.

Fig. 2 provides an alignment of heat shock proteins from a variety of organisms: 1. M.hyopneumoniae (Mhyhsp70 - R03922);

S. Bacillus megaterium (Bmhsp70 - R03922);

C. Bacillus megaterium (Bmhsp70 - R03922);

C. T. cruzi (tc70kd - R03924);

C. T. cruzi (tc70kd - R03925);

C. T. cruzi (tc70kd - R03928);

C. T. cruzi (tc70kd - R03928);

C. T. cruzi (tc70kd - R03928);

C. Set rattus (rathsp70 - R03929);

C. Se Homo saplens (humhsp70 - R03929);

C. D. Zea mays (mzehsp70 - R03931);

C. Lio Zea mays (mzehsp70 - R03931);

C. Lio Zea mays (mzehsp70 - R039321).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
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                                                                                                                                                                                                                        The likelihood of mammalian fertilisation is decreased by contacting a gamete with a sulphoglycolipid immobilising protein 1 (SLIP1)/ sulphated glyco-molety interfering composition. The interfering compas. Is e.g. the heat shock 70kD protein, SLIP1 (or analogues such as the mouse SLIP1 analogue "HSC70B" comptrising the analogue sequence R43002) or the 74.5kD mycoplasma protein (R43003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ij
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                                                                                             Mammalian fertilisation decrease for detecting and treating infertility - uaing sulpho glyco lipid immobilising protein 1-sulphated-glyco molety interfering compsn., for mycoplasma infection treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-AUG-1990 (first entry)
Gallus gallus HSP (chkhsp70).
Hsp70; heat shock protein; Trypanosoma cruzi; vaccines; HSP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.8%; Score 82; DB 5; Length 634; 26.3%; Pred. No. 1.11e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 12.9%; Score 83; DB 8; Length 641; Local Similarity 26.3%; Pred. No. 9.13e+00; Conservative 12; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            264 rtacerakrtlssstgasleidslfegidfytsitrar 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note- "residue given as "O" in specification" W09002564-A.
(OTTA-) OTTAWA CIVIC HOSPITAL.
Faulds DH, Lingwood CA, Tanphaichitr N;
WPI; 93-368422/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R03930 standard; Protein; 634 AA.
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WPI; 90-115820/15.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-SEP-1989; 03955.
12-SEP-1988; US-243474.
(CODO-) Codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacteria species.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              641 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              634 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gallus gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
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Gaps

4

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protein sequences (Talm 1) Page 8-9; 13pp; Japanese.

The enzymes (R66729-34), encoded by genes 079907-12, are involved in the synthesis of dihydrodiol and catechol compounds by microbial fermentation in E.coll at normal temps. and pressures from aromatic Phydrocarbons.

The sequence presented here its of an aromatic deoxygenese of 459 amino acids. The aromatic dihydrodiol can be used as a raw material for engineering plastics and the catechol compound is used as a polymerisation inhibitor of synthetic resin and as an intermediate in drug synthesis.
02-001-1995 (first entry)
Aromatic dihydrodiol/catechol deoxygenase #1.
Dihydrodiol; catechol; microbial fermentation; E.coll; aromatic;
deoxygenase; hydrocarbon; engineering plastic; polymerisation inhibitor;
synthetic resin; drug synthesis.
Pseudomonas fluorescens SD805.
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Pred. No. 1.34e+01;
13; Mismatches 26; Indels
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Sednence Query Match

Best Loca Matches

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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding human calcium channel sub-unit(s) - used for developing prods. for studying calcium channels, e.g. for obtaining agonists and antagonists

Claim 34; Page 178-190; 285pp; English.

Claim 34; Page 178-190; 285pp; English.

The primary transcelpt of the alpha 1A subunit gene is alternatively spliced to yield at least two variant mRNAs.

Claim 34; Page 178-190; 285pp; English.

The primary transcelpt of the alpha 1A subunit gene is alternatively spliced to yield at least two variant mRNAs.

Claim 34: Page 178-190; 285pp; English.

The pha 1A-1 encoding sequence at the 3' end in that it lacks a star as a translation termination codon resulting in an introduces a translation termination codor resulting in an alpha 1A-2 coding sequence that encodes a shorter alpha 1A introduces at translation termination codor resulting in an alpha 1A subunits can be isolated using all A-1. DNA doncding alpha 1A subunit that has been deposited in the ATCC under accession to 75593. The DNA is such a phage includes the DNA fragment having the sequence in Q84661 which selectively hybridises under to but the phage in this stringency to DNA encoding alpha 1A DNA but not
Gaps
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N-PSDB; 076209.
N-PSDB; 076209.
- for inhibiting HSV L/ST synthesis, in the treatment of HSV
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                                                                                                                                                                                                                                                                                                               16-FEB-1995.
11-ANG-1994 U09230.
11-ANG-1993; US-149097.
(SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
Ellis SB, Gillespie A, Harpold MM, Mccue AF, Williams ME; 95-090900/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 81; DB 14; Length 2510;
Pred. No. 1.34e+01;
12; Mismatches 18; Indels
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Herpes simplex virus type 1.
WO9428156-A.
                                                                                                                                                                             01-DEC-1995 (first entry)
Human neuronal calcium channel subunit alpha 1A-1.
Calcium channel subunit; antagonist; agonist; diagnosis;
Lambert Eaton Syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2235 agerpdhgrarardgrwsrspsegrehmahrggsssvsgspaps 2278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-DEC-1994.
20-MAY-1994; U05770.
20-MAY-1993; US-065146.
CDAND ) DANA FARBER CANCER INST INC.
Schaffer PA, Yeh L;
                                                                                                                T 12
R71007 standard; Protein; 2510 AA.
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R64327 standard; Protein; 233 AA.
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Best Local Similarity 31.8%;
Matches 14; Conservative
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quence 2510 AA;
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WO9504822-A.
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Overlapping clones, which make up the CDNA sequence from which this sequence was deduced, were isolated from a murine PBL CDNA library prepared in lambda gt10. The purified protein can mediate the cytolytic activity of mammalian cells. It specifically distinguishes tumour cells making it a candidate for the development of products for the immunodetection and immunotherapy of tumours.
                                                                                                                                                                                                                               Gaps
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In HSV-1, 4 intron-less open reading frames (ORFS) are present within the sequence specifying the L/ST junction-spanning transcript. ORF1-4 are given in Q76209-12, and encoded proteins in R64327-30. Antibodies raised against such proteins may be used to identify therapeutic agents.
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Pred. No. 1.62e+01;
12; Mismatches 14;
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12.4%; Score 80; DB 3; Lu
Best Local Similarity 38.2%; Pred. No. 1.62e+01;
Matches 13; Conservative 9; Mismatches 8.
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R13319 standard; Protein; 1023 AA
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R13320 standard; Protein; 982 AA.
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08-JUN-1990; 08-535206.
(USSH) NMT INST OF HEALTH.
Ortaldo J, Young H, Anderson S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= partial_signal_peptide US7535206-A.
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Ortaldo J, Young H, Anderson
WPI; 91-245694/33.
N-PSDB; Q13114.
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Best Local Similarity 32.5%;
Matches 13; Conservative
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/label= mature_NK_receptor
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N-PSDB; Q13115.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein
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prods. for the immuno-detection and immuno-therapy of tumours Disclosure; Fig 1; 30pp; English.
Overlapping clones, which make up the cDNA sequence from which this sequence was deduced, were isolated from a cDNA library prepared from human NK cells purified from human peripheral blood. The purified protein can mediate the cytolytic activity of mammalian cells. It specifically distinguishes tumour cells making it a candidate for the development of products for the immunodetection and immunotherapy of tumours. See also Qi3115.
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4 Gaps 4, Query Match 12.4%; Score 80; DB 3; Length 1023; Bost Local Similarity 38.2%; Pred. No. 1.62e+01; Matches 13; Conservative 9; Mismatches 8; Indels

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Wed Aug 20 11:09:01 1997; MasPar time 5.05 Seconds 503.601 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-320-157-21 (1-88) from US08320157.pep 643 1 MASGQGPGPPRQECGKPALP......APWGRWDGSSPSPGRHQPAL 88 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

91006 segs, 28888923 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir51
1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3
8:unann4 9:unann5 10:unann6 11:unann7 12:unann8
13:unann9 14:unann10 15:unenc 16:unrev

Mean 37.327; Variance 80.459; scale 0.464 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Pred. No.	.18e-20	18e-20	.35e-01	.82e-01	.84e+00	43e+00	2.43e+00	.21e+00	.21e+00	.21e+00	.21e+00	21e+00	.21e+00	.21e+00	.21e+00	.21e+00	.23e+00	.23e+00	.23e+00	.23e+00	23e+00
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SUMMARIES	Ω	S58875	S58873	A40623	S37577	209036	S18156	A36333	A48872	S20139	S37394	HHBYA1	S25585	HHXL70	S18349	S26369	B35098	B44261	B47092	JC1495	S10235	S31766
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A29160 156574 154542 A45871 335718 347098 A40098 A61181 A61181 A61181 151129 JGA86 A64786 A64786 A64786 A63309 JGA86 A63309 JGA86 A63309 JGA86 A63309 JGA86 A63309 JGA86 A63309 JGA86 A63309 JGA86 A63309 JGA86 A63309 JGA86 A63309 JGA86 A63309 JGA86 A63309 JGA86 A63309 JGA86 A63309 JGA86 A63309 JGA86 A63309 JGA86 A63309 JGA86 A63309 JGA86 A63309 JGA86 JGA	LIGNMENTS  complete human no sapiens #c quence_revisi quence_revisi duence_revisi sauer, M.J.; .D.; Barr, P. 4:736-739 optosis by t 4:736-739 optosis by t con not shown el KIE 18812 inucleic ac not shown el KIE 18812 inucleic ac no not shown el KIE inucl	Score 213; Pred. No. 9 2; Mismarc Seeqvaddteevi
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222 224 232 233 233 233 233 233 233 233	RESULT 1 ENTRY TITLE ORGANISM DATE ACCESSIONS REFERENCE #authors #journal #title #accession #status ##residues ##residues ##residues ##note SUMMARY	Query Match Best Local Si Matches 32 Db 1 masgg Qy 1 MASGQ RESULT 2 ENTRY TITLE ALTERNATE_NAMES ORGANISM DATE ACCESSIONS REFERENCE #authors #journal #title

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Nature (1995) 374:736-739
Modulation of apoptosis by the widely distributed Bcl-2
homologue Bak.
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                                                                                                                        Farrow, S.N.; White, J.H.M.; Martinou, I.; Raven, T.; Pun, K.T.; Grinham, C.J.; Martinou, J.C.; Brown, R. Nature (1995) 374:731-733 Cloning of a bcl-2 homologue by interaction with adenovirus
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heat shock protein Y - Escherichia coli
#formal_name Escherichia coli
21-589-1993 *sequence_revision 18-Nov-1994 *text_change
15-Nov-1996
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Missiakas, D.; Georgopoulos, C.; Raina, S.
Missiakas, D.; Georgopoulos, C.; Raina, S.
The Bacterioli. (1993) 175:2613-2624
The Escherichia coli heat shock gene htpY: mutational analysis, cloning, sequencing, and transcriptional
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DNA Seq. (1993) 3:327-332
Five open reading frames upstream of the dnaK gene of
Escherichia coli.
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:Y #length 211 #molecular-weight 23409 #checksum 801
##molecule_type mRNA
##rolecule_type mRNA
##rosidues 1-211 ##label CHI
##cross-references EMBL:U23765
:NCE $55872
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##cross-references NCBIN:130422; NCBIP:130423
##note sequence extracted from NCBI backbone
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Best Local Similarity 78.0%; Pred. No. 9.18e-20;
Matches 32; Conservative 2; Mismatches 6;
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                                                                                                                                                                                                             ##molecule_type mRNA
##residues
1-211 ##label FAR
##cross-references EMBL:X84213
REFERENCE $58874
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*cross-references MUID:93239687
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The human heat-shock protein family. Expression of a novel heat-inducible HSP70 (HSP70B') and isolation of its cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SU9036 *type complete heat shock protein 70B' - human *formal_name Homo sapiens *common_name man 30-Sep-1991 *sequence_revision 30-Sep-1991 *text_change 06-Sep-1996
                                                                                                                                               Gaps
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Shb protein - human
#formal_name Homo sapiens #common_name man
06-Jan-1995 *sequence_revision 06-Jan-1995 *text_change
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0 min
heat shock; stress-induced protein
#length 196 #molecular-weight 21225 #checksum 5329
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Y #length 596 #molecular-weight 64525 #checksum 5363
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#map_position 1cen-1qter
CLASSIFICATION #superfamily heat shock protein 70
SUMMARY #length 643 #molecular-weight 70853 #checksum 313
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submitted to the EMBL Data Library, October 1993
837577
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                                                                                             Score 95; DB 9; Length 196;
Pred. No. 1.35e-01;
2; Mismatches 7; Indels
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*#residues 1-643 #*label LEU
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#accession S09036
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                                                                                          Query Match 14.8%;
Best Local Similarity 57.1%;
Matches 12; Conservative
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##residues 1-59
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A2647, R.J.; Sauterer, R.A.; Condeelis, J.S.
J. Biol. Chem. (1993) 266:23267-23374
Aginactin, an agonist-regulated F-actin capping activity is
                                   globulin 1 - eastern white pine
#formal_name Pinus strobus #common_name eastern white pine
6-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
06-Jan-1995
$18156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #authors Perkins, L.A.; Doctor, J.S.; Zhang, K.; Stinson, L.;
Perrimon, N.; Craig, E.A.
#journal Mol. Cell. Biol. (1990) 10:3232-3238
#title Molecular and developmental characterization of the heat shock cognate 4 gene of Drosophila melanogaster.
#cross-references MUID:90258915
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70k heat shock cognate protein aginactin - slime mold
(Dictyostelium discoideum) (fragment)
F-actin capping protein aginactin
#formal_name Dictyostelium discoideum
19-May-1995 #sequence_revision 19-May-1995 #text_change
03-May-1996
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25-Jan-1991 #sequence_revision 25-Jan-1991 #text_change
12-Apr-1995
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heat shock cognate protein 70 - fruit fly (Drosophila
melanogaster)
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##cross-references EMBL:211486
Y #length 488 #molecular-weight 54715 #checksum 3250
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#length 651 #molecular-weight 71059 #checksum 805
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                                                                                                                                        Rugh, C.L.; Kamalay, J.C.
submitted to the EMBL Data Library, November 1991
                                                                                                                                                                                                                                                                                                                               Length 488;
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13.2%; Score 85; DB 7; Length 651;
Best Local Similarity 26.3%; Pred. No. 2.43e+00;
Matches 10; Conservative 13; Mismatches 14; Indels
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Pred. No. 2.43e+00;
7; Mismatches 14; Indels
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Best Local Similarity 36.1%;
Matches 13; Conservative
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Purnelle, B.; Goffeau, A. submitted to the EMBL Data Library, April 1996

The sequence of 32 kb on the left arm of yeast chromosome XII reveals 14 open reading frames among which HSP104, SSA2, SPA2, KNS1, DPS1/ARS, SDC25, a new member of the seripauperins family and a new ABC transporter homologous to the human multidrug resistance protein.
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                                                                                                                                 residue 10 as Pro,
residue 350 as Thr,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                $20139 #type complete heat shock protein $SA2 - yeast (Saccharomyces cerevisiae heat shock protein $SA2 - yeast (Saccharomyces cerevisiae heat shock protein YGL024c #formal_name Saccharomyces cerevisiae 07-may-1993 #sequence_revision 07-may-1993 #text_change
                                                                                                                                                                                                                                                                                                             Gaps
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submitted to the Protein Sequence Database, May 1996
S64772
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Nucleic Acids Res. (1989) 17:805-806
The SSAl and SSA2 genes of the yeast Saccharomyces
Cerevisiae.
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associated with an Hsc70 in Dictyostelium.
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                                    258 rtacerakrtlsssaqasieidslfegidfytsitrar 295
                                                                                                                                                                                                                                                                                                                                                                               #superfamily heat shock protein 70
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S20139; S64772; S64775; S69383
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##rosidues 72-639 ##label DUE
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NCE S64775
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##experimental_source strain S288C
SNCE S69380
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##cross-references EMBL:X12927
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##molecule_type DNA
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##molecule_type DNA
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##residues 1-63
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#cross-references MUID:89128457
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Clark, M.W.; Keng, T.; Storms, R.K.; Zhong, W.; Fortin, N.;
Zeng, B.; Delaney, S.; Ouellette, B.F.F.; Barton, A.B.;
Kaback, D.B.; Bussey, H.
Yeast (1994) 10:535-541
Sequencing of chromosome I of Saccharomyces cerevisiae:
analysis of the 42 kbp SPO7-CENI-CDC15 region.
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#type complete

theat shock protein SSA1. yeast (Saccharomyces cerevisiae)

heat shock protein 70-related protein SSA1; heat shock

protein YG100; protein YAL005c

protein YG100; protein YAL005c

#formal_name Saccharomyces cerevisiae

36-Jun-1993 #sequence_revision 30-Jun-1993 #text_change

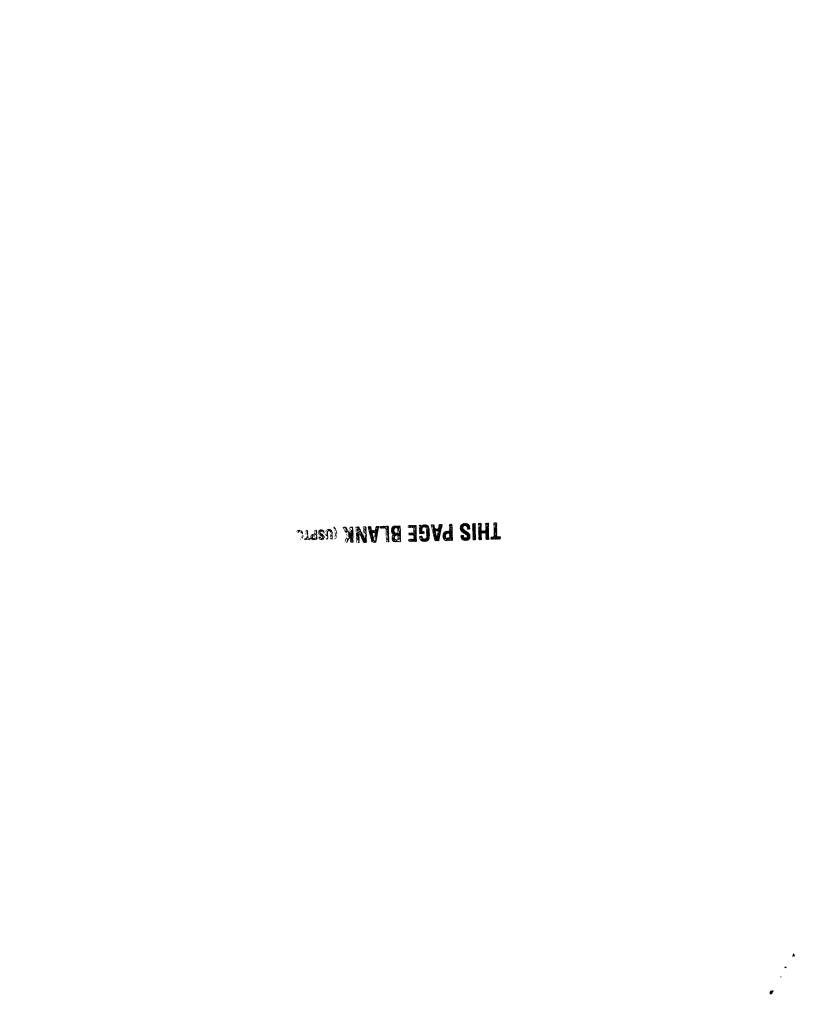
15-Nov-1996
                                                                                                                                                                                                                                                                                                                                                                           Haus, U.; Trommler, P.; Fisher, P.R.; Hartmann, H.;
Lottspeich, F.; Noegel, A.A.; Schleicher, M.
EMBO J. (1993) 12:3763-3771
The heat shock cognate protein from Dictyostellum affects
actin polymerization through interaction with the
actin-binding protein cap32/34.
                                                                                                                                                                                                                                  S37394 *type complete
heat shock cognate protein 70 - slime mold (Dictyostelium
                                                                                          Gaps
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#formal_name Dictyostelium discoideum
31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
12-Apr-1995
 molecular chaperone
#length 639 #molecular-weight 69469 #checksum 5309
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*length 640 *molecular-weight 70499 *checksum 4857
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                                                  Score 84; DB 7; Length 639;
Pred. No. 3.21e+00;
12; Mismatches 15; Indels
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13.1%; Score 84; DB 7; Length 640;
Best Local Similarity 26.3%; Pred. No. 3.21e+00;
Matches 10; Conservative 12; Mismatches 15; Indels
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##note the nucleotide sequence was submitted
Library, November 1993
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##cross-references EMBL:X75263
                                                  Query Match
Best Local Similarity 26.3%;
Matches 10; Conservative
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##molecule_type DNA
##residues 1-207,'S',209-417,'P',419-421,'S',423-642 ##label SL2
##cross-references EMBL:X13926
##note this is a revision to the sequence from reference S20139
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heat shock protein 70 - African clawed frog
heat shock protein 716
#formal_name Aenopus laevis #common_name African clawed frog
28-May-1986 #sequence_revision 28-May-1986 #text_change
15-Nov-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dezeure, F.; Vaiman, M.; Chardon, P.
Biochim. Biophys. Acta (1993) 1174:17-26
Characterization of a polymorphic heat shock protein 70 gene
in swine outside the SLA major histocompatibility complex.
S34625
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heat shock protein 70 - pig
#formal_name Sus scrofa domestica *common_name domestic pig
#formal_pame Sus scrofa domestica *common_name domestic pig
03-Rug-1995 *sequence_revision 20-Feb-1995 *text_change
03-Rug-1995
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CLASSIFICATION #superfamily heat shock protein 70
SUMMARY #length 643 #molecular-weight 71109 #checksum 9470
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submitted to the EMBL Data Library, June 1993
S42164
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13.1%; Score 84; DB 3; Length 642;
Best Local Similarity 26.3%; Pred. No. 3.21e+00;
Matches 10; Conservative 12; Mismatches 15; Indels
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##molecule_type DNA
##residues 1-642 ##label SLA
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##residues
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A90993
Bienz, M.
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S25438
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Search completed: Wed Aug 20 11:09:37 1997 Job time: 36 secs.
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EMBO J. (1984) 3:2477-2483
Xenopus hsp 70 genes are constitutively expressed in injected
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                                                                                                                                                                           #authors Bienz, M.
#journal Proc. Natl. Acad. Sci. U.S.A. (1984) 81:3138-3142
#fille Developmental control of the heat shock response in Xenopus.
#cross-references WUID:84221917
#accession A22175
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genome polyprotein - eastern equine encephalomyelitis virus
nonstructural protein NS1: nonstructural protein NS2;
nonstructural protein NS3
nonstructural protein NS3
005-Lan=1994 #sequence_revision 01-Nov-1996 #text_change
01-Nov-1996
                                                                                                                                                                                                                                                                                                                          This protein is expressed constitutively in occytes, disappears after fertilization, and is induced by heat shock in somatic cells from the gastrula stage onward.

TION *superfamily heat shock protein 70 heat shock; molecular chaperone; stress-induced protein *length 647 *molecular-weight 70915 *checksum 3965
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heat shock protein 70 - carrot
#formal_name Daucus carota #common_name carrot
04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change
12-Apr-1995
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CLASSIFICATION #superfamily heat shock protein 70
SUMMARY #length 655 #molecular-weight 72051 #checksum 2153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #authors Lin, X.; Chern, M.; Zimmerman, J.L.
#journal Plant Mol. Biol. (1991) 17:1245-1249
#title Cloning and characterization of a carrot hsp70 gene.
#cross-references MUID:92032789
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Complete nucleotide sequence of the eastern equine encephalomyelitis virus genome.
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Pred. No. 3.21e+00;
14; Mismatches 9; Indels
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Pred. No. 3.21e+00;
12; Mismatches 15; Indels
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                                                                                                                                                                                                                                                                              ##molecule_type mRNA
##residues 81-120 ##label BI2
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##residues 1-655 ##label LIN
                                                                                                   ##molecule_type DNA
##residues 1-647 ##label BIE
                                     cocytes.
#cross-references MUID:85076567
#accession A03310
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Best Local Similarity 26.3%;
Matches 10; Conservative
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Best Local Similarity 30.6%;
Matches 11; Conservative
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S18349
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KEYWORDS
SUMMARY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #journal
#title
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REFERENCE
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ORGANISM
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4,
                                                                                       sequence could not be checked because of bad print in
                                                                                                                                                                            #product nonstructural protein NS1 #status predicted
#label NS1\
#product nonstructural protein NS2 #status predicted
#label NS2\
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                                                                                                                                                                                                                                                                                                                                                                                                                                        #checksum 5340
                                                                                                                                                                                                                                                                                                                                                 Query Match 13.1%; Score 84; DB 8; Length 1878; Best Local Similarity 33.9%; Pred. No. 3.21e+00; Matches 19; Conservative 14; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                            #molecular-weight 208582
                                                                                                                                nonstructural protein; polyprotein
#accession S26369
##molecule_type mRNA
##residues 1-1878 ##label VOL
##cross-references EMBL:X63135
##note
                                                                                                                                                                                                                                                              #product nons
#label NS3
#length 1878 #mo
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Wed Aug 20 11:09:54 1997; MasPar time 3.60 Seconds 517.994 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-320-157-21 (1-88) from US08320157.pep 643 Title: Description: Perfect Score:

1 MASGQGPGPPRQECGKPALP.....APWGRWDGSSPSPGRHQPAL 88 Sequence:

PAM 150 Gap 11 Scoring table:

59021 seqs, 21210388 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

swiss-prot34 Database:

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 Mean 38.620; Variance 68.467; scale 0.564 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	& Query Match	Length DB	80	ΩI	Description		Pred. No.
H	95	14.8	196	. 2	HTGA ECOLI	SHOCK	PROTEIN HT	1.666-02
7	98	13.4	643	S	HS76_HUMAN		œ	3.58e-01
e	85	13.2	651	S	HS7D_DROME		KD PROT	4.97e-01
4	84	13.1	379	Ŋ	HS7X_PIG		KD PROT	6.89e-01
S	84	13.1	631	S	HS73_BOVIN	-	KD PROT	6.89e-01
9	84	13.1	638	S	HS72_YEAST	SHOCK	PROTEIN SS	6.89e-01
7	84	13.1	640	'n	HS7C_DICDI	SHOCK		6.89e-01
œ	84	13.1	641	ហ	HS71_YEAST	SHOCK	PROTEIN SS	6.89e-01
σ	84	13.1	643	ഗ	HS76_PIG	HEAT SHOCK 70	24	6.89e-01
10	84	13.1	647	ហ	HS70_XENLA		KD PROT	6.89e-01
11	84	13.1	649	ഗ	HS70_BLAEM		KD PROT	6.89e-01
12	84	13.1	655	'n	HS70_DAUCA	HEAT SHOCK 70	ΚΩ	6.89e-01
13	84	13.1	2142	Н	BAT2_HUMAN	LARGE PROLINE-RICH	-RICH PR	6.89e-01
14	83	12.9	284	4	GOLI_DROME	GOLIATH PROTEIN (	G	9.52e-01
12	83	12.9	462	4	FUCO_RAT	ALPHA-L-FUCOSI	IDASE PR	9.52e-01
16	83	12.9	641	S	HS71_HUMAN	HEAT SHOCK 70	KD PROT	9.52e-01
17	83	12.9	641	'n	HS71_PIG	HEAT SHOCK 70	KD PROT	9.52e-01
18	83	12.9	641	S	HS71_RAT		KD PROT	9.52e-01
19	83	12.9	642	Ŋ	HS71_MOUSE	HEAT SHOCK 70	ξÃ	9.52e-01
20	83	12.9	642	S	HS72_PICAN	HEAT SHOCK PRO	PROTEIN 70	9.52e-01
21	83	12.9	2647	<del>1</del>	ABP2_HUMAN	ENDOTHELIAL AC	ACTIN-BIN	9.52e-01
22	82	12.8	634	Ŋ	HS70_CHICK	HEAT SHOCK 70	KD PROT	1.31e+00

1.31e+00 1.31e+00 1.31e+00 1.31e+00 1.80e+00 1.80e+00 1.80e+00 1.80e+00 2.47e+00 2.47e+00 2.47e+00 2.47e+00 2.47e+00 2.47e+00 3.38e+00 3.38e+00	3.38e+00
HEAT SHOCK 70 KD PROT RIBONUCLEOSIDE-DIPHOS HELICASE/PRIMASE COMP COLLAGEN ALPHA 1 (XIV) HEAT SHOCK 70 KD PROT HEAT SHOCK 70 KD PROT PROBABLE HEAT SHOCK P PROBABLE HEAT SHOCK P NK-TUMOR RECOGNITION KK-TUMOR RECOGNITION KK-TUMOR RECOGNITION KK-TUMOR RECOGNITION HYPOTHETICAL 45.1 KD HEAT SHOCK-RELATED 70 HEAT SHOCK-RELATED 70 HEAT SHOCK-RELATED 70 HEAT SHOCK-RELATED 70 HEAT SHOCK-RELATED 70	HEAT SHOCK COGNATE 70
H574_PARLI RIRI_HSVBC CUI52_EBV CUI52_EBV H574_DROSI H570_DROWE H570_ROWE H570_ROWE H571_BROWE H571_BROWE H571_BROWE H571_BCOME H571_BCOME H571_LSCHPO H571_LSCHPO H571_LSCENP	HS7C_PETHY
110 110 110 110 110 110 110 110 110 110	S
0 / 4 8 4 / H 4 4 H 8 8 4 0 M 8 9 0 M 8 8 8	651
	12.3
7 7 7 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	73
24222222222222222222222222222222222222	45

#### ALIGNMENTS

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HTGA OR HTPY.

ESCHERICHIA COLI.

PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
ENTEROBACTERIACEAE.
                 01-DEC-1992 (REL. 24, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
HEAT SHOCK PROTEIN HTGA (HEAT SHOCK PROTEIN HTPY).
       196 AA
                                                                                               [2]
SEQUENCE FROM N.A.
STRAIN=K12 / WAILIO,
MEDILIS 93239687.
MISSIAKAS D., GEORGOPOULOS C., RAINA S.;
J. BACTERIOL. 175:2613-2624(1993).
       PRT;
                                                                                     DEBBAGE J.;
       STANDARD;
                                                                       SEQUENCE FROM N.A.
MEDLINE; 94003405.
JAMES R., DEAN D.O., DEB
DNA SEQ. 3:327-332(1993)
RESULT 1
ID HTGA_ECOLI
AC P28697;
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GENE 128:155-163(1993).
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ID HS7X_PIG
AC P34934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
CONFLICT
CONFLICT
SEQUENCE
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01-JUL-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-JWN-1994 (REL. 29, LAST ANNOFATION UPDATE)
01-JWN-1994 (REL. 29, LAST ANNOFATION UPDATE)
11-JWN-1994 (REL. 29, LAST ANNOFATION U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSPAG OR HSP70B'.
HOMO SAPTENS (HUMAN).
BURAKYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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BODLINE; 93292982.
RUBIN D., MEHTA A., ZHU J., SHOHAM S., CHEN X., WELLS Q.,
PALTER K.B.;
                                                                              Score 95; DB 5; Length 196;
Pred. No. 1.66e-02;
2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 26.8%; Pred. No. 3.58e-01;
Matches 11; Conservative 12; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    01-AGG-1990 (REL. 15, CREATED)
01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
HEAT SHOCK 70 KD PROTEIN 6 (HEAT SHOCK 70 KD PROTEIN B').
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C., LIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 263 grlrtacerakrtlssstgatleidslfegvdfytsitrar 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 GPPRQECGKPALPSASEEQVAQDMEG-FSAATFFTTISRNR 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-LUNG;
MEDILINE; 90226304.
LEUUG T.K.C., RAJENDRAN M.Y., MONFRIES C., HALL
BIOCHEM. J. 267:125-132(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WIM: 14035;
PROSITE: PS00297; HSP70_1.
PROSITE: PS01036; HSP70_3.
PROSITE: PS01036; HSP70_3.
ATP-BINDING; HEAT SHOCK; MULTIGENE FAMILY.
SEGUIENCE 643 AA; 70854 MW; D7C64887 CRC32;
                             D9E3CEC8 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             651 AA.
                                                                                                                                                                                                                                                                                                                                                                      643 AA
     POLY-SER
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                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65
21225 MW;
                                                                                                                                                                                                   14 ppspaprskpcpstliaawvr 34
                                                                                                                                                                                                                                   53 PPLPTQRWSPCPSNLAAPWGR 73
                                                                                    h 14.8%;
Similarity 57.1%;
12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P19120; INGA.
HSC-2DPAGE; P17066; HUMAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
57
196 AA;
                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                      RESULT 2

HEAT HUMAN

AC 01-AGG-1990

DT 01-FBG-1990

DT 01-FBG-1990

DT 01-FBG-1990

DT 01-FBG-1990

DT HEAT SHOCK 7

GN HSPA6 OR HSP

CS BUKARYOTA, M

COC EUTHERIA; PR

RN (12)

RN (12)

RN (12)

RD HSDLINE; 902

RA BEDLINE; 903

RA BEDLINE; 903

RA BEDLINE; 903

RA BEBLI, X51758

DR EMBL; S79631

DR RESSP; P99036;

DR RSSP; P99036;

DR PROSITE; PS0

DR PROSITE; PS0

DR PROSITE; PS0

KW ATP-BINING;

SEQUENCE 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LT 3
HS7D_DROME
  DOMAIN
SEQUENCE
                                                                                       Query Match
                                                                                                                                        Matches
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01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
HEAT SHOCK 70 KD PROTEIN (FRAGMENT).
SUS SCROFA (PIG).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
[2]
SEQUENCE FROM N.A.
MEDLINE; 90258915.
PERKINS L.A., DOCTOR J.S., ZHANG K., STINSON L., PERRIMON N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00297; HSP70_1.
PROSITE; PS003297; HSP70_2.
PROSITE; PS01039; HSP70_2.
ATP-BINDING; HEAT SHOCK; NUCLEAR PROTEIN; MULTIGENE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 85; DB 5; Length 651;
Pred. No. 4.97e-01;
13; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-KIDNEY;

MEDLINE; 90374627.

BUCHANA T. G., CABIN D.E., VICKERS S.;

SURGERY 108:559-566(1990).

-1. SINILARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.

EMBL; M29506; G164495; -.

HSSP; P19120; 1NGA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       167 L -> P (IN REF. 2)
170 L -> P (IN REF. 2)
625 P -> G (IN REF. 2)
71131 MW; 75CC8721 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      264 rtacerakrtlssstgasieidslfegtdfytsitrar 301
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PROSITE; PS00329; HSP70_2.
PROSITE; PS01036; HSP70_3.
ATP-BINDING; HEAT SHOCK; MULTIGENE FAMILY.
NON_TER
                                                                                                                                                                                                                                                   [3]
SEQUENCE OF 1-104 FROM N.A.
SEQUENCE 84005511.
CRAIG E.A., INGOLIA T.D., MANSEAU L.J.;
DEV. BIOL. 99:418-426(1983).
                                                                                                                                                                        CRAIG E.A.;
MOL. CELL. BIOL. 10:3232-3238(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P19120; 1ATR.
FLYBASE; FBGN0001219; HSC70-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 26.3%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               651 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1]
SEQUENCE FROM N.A.
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GARRELS J. I., FUTCHER B., KOBAYASHI R., LATTER G.I., SCHWENDER B., VOLRE T., WARNER J. R., MCLAGGLIN C.S.;
SUBMITTED (SEP.1994) TO THE SWISS-PROT DATA BANK.
-!- FUNCTION: SSA2 MAY PLAY A ROLE IN THE TRANSPORT OF POLYPEPTIDES BOTH ACROSS THE MITOCHONDRIAL MEDRANES AND INTO THE ENDOPLASMATIC RETICULUM. A FUNCTIONAL DIFFERENCE BETWEEN YEAST SSA1 AND SSA2 PROFEINS IS EXECTED. SSA2 CAN PARTICIPATE IN THE ATP-DEPENDENT DISASSEMBLY OF CLATHRIN-COATED VESICLES.
                         SEQUENCE OF 71-638 FROM N.A.
DUESTERHOEFT A., FLOETH M., HEUSS-NEITZEL D., HILBERT H., MOESTL
SUBMITTED (MAY-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                             SEQUENCE OF 91-97 AND 325-341.
STRAIN-S2BBC;
MEDLINE; 95203288.
GARRELS J.I., FUTCHER B., KOBAYASHI R., LATTER G.I., SCHWENDER VOLPE T., WARNER J.R., MCLAUGHLIN C.S.;
ELECTROPHORESIS 15:1466-1486(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-AX3;
MEDLINE: 94008983.
HAUS U., TROMMLER P., FISHER P.R., HARTMANN H., LOTISPEICH F.,
NOEGEL A.A., SCHLEICHER M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EUKARYOTA; PROTOZOA; SARCOMASTIGOPHORA; SARCODINA; RHIZOPODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 84; DB 5; Length 638;
Pred. No. 6.89e-01;
12; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- PTM: PHOSPHORYLATED.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
-!- SIMLARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.
EMBL; X12927; 64546; -.
EMBL; Z73129; E245749; -.
EMBL; X7560; E228712; -.
PIRS, S20139; S20139.
SWISS-ZDPAGE; P10592; YEAST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HEAT SHOCK; ATP-BINDING; MULTIGENE FAMILY; ACETYLATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACETYLATION.
676F4EE3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1994 (REL. 29, CREATED)
01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ş
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DICTYOSTELIUM DISCOIDEUM (SLIME MOLD)
                                                                                                                                                                                                                                                                                           STRAIN-ATCC 38531 / Y41;
NORBECK J., BLOMBERG A.;
FEMS MICROBIOL. LETT. 137:1-8(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69338 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 13.1%;
Best Local Similarity 26.3%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGD; L0002070; SSA2.
PROSITE; PS00297; HSP70_1.
PROSITE; PS00329; HSP70_2.
PROSITE; PS01036; HSP70_3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EUMYCETOZOA; DICTYOSTELIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                          SEQUENCE OF 186-195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                638 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PHOSPHORY LATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSPB OR HSC70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HS7C_DICDI
P36415;
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MOD_RES
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RA SEQUENCE FROM N.A.

RA GROSZ M.D., MASSEY V.K., SKOW L.C.;

ROSZ M.D., MASSEY V.K., SKOW L.C.;

RE SUBMITTED (XXX-1992) TO EMBL/GENBANK/DDBJ DATA BANKS.

CC -I- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE PRESESTSTENT PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN CC OF NEWLY TRANSLATED POLYPEPTIDES IN ALL THESE PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF OTHER PROTEINS. THESE EXPOSED BY POLYPEPTIDES DURING TRANSLATION OF FOLLOWING STRESS-INDUCED DAMAGE.

CC HYDROPHORIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION OR FOLLOWING STRESS-INDUCED DAMAGE.

CC -I- SIMILARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.

DR REMBL: L10428 1 G153161; --

DR ROSSITE; PS00029; HSP70_1.

DR PROSITE; PS000329; HSP70_2.

DR PROSITE; PS01036; HSP70_2.

DR PROSITE; PS01036; HSP70_2.

EMBL: L10428 1 ASP70_2.

DR PROSITE; PS01036; HSP70_2.

EMBL: L10428 1 ASP70_2.

EMBL: L10428 1 ASP70_2.

DR PROSITE; PS01036; HSP70_2.

EMBL: L10428 1 ASP70_2.

EMBL: L10428 1 ASP70_2.

EMBL: L10428 1 ASP70_2.

DR PROSITE; PS01036; HSP70_2.
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                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                         BOS TAURUS (BOVINE).
EUKARXOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                             ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 84; DB 5; Length 631;
Pred. No. 6.89e-01;
15; Mismatches 17; Indels
                                              Score 84; DB 5; Length 379;
Pred. No. 6.89e-01;
12; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-S288C;
PURNELLE B., GOFFEAU A.;
SUBMITTED (APR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   257 aparlrtacerakrtlssstgasieidslyegvdfytsitrar 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSAZ OR YLL024C OR L0931.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
                                                                                                                                     41
                                                                                                                                                          9E26ABE8 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-001-1989 (REL. 11, CREATED)
01-0CT-1994 (REL. 30, LAST SEQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
HEAT SHOCK PROTEIN SSA2.
                                                                                                                                                                                                                                                                                                         01-FEB-1994 (REL. 28, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
                                                                                                                              4 rtacerakrtlssstqatleidslfegvdfytsitrar
                                                                                                                                                                                                                                                                      631 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-S288C;
MEDLINE; 89128457.
SLATER M.R., CRAIG E.A.;
NUCLEIC ACIDS RES. 17:805-806(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                      PRT;
  42289 MW;
                                            Query Match 13.1%;
Best Local Similarity 26.3%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          V Match
Local Similarity 23.3%;
hes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                             HEAT SHOCK 70 KD PROTEIN 3
                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EUTHERIA; ARTIODACTYLA
379 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                           5
HS73_BOVIN
P34933;
01-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HS72_YEAST
P10592;
  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                         HSP70-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Gaps

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GARRELS J.I., FUTCHER B., KOBAYASHI R., LATTER G.I., SCHWENDER B., VOLPE T., WARNER J.R., MCLAUGHLIN C.S.;
SUBMITTED (SEP-1994) TO THE SWISS-PROT DATA BANK.
-!- FUNCTION: SSA1 MAY PLAY A ROLE IN THE TRANSPORT OF POLYPEPTIDES BOTH ACROSS THE MITOCHONDRIAL MEMBRANES AND INTO THE ENDOPLASMATIC RETICULUM. A FUNCTIONAL DIFFERENCE BETWEEN YEAST SSA1 AND SSA2 PROTEINS IS PRECTED. SSA1 CAN PARTICIPATE IN THE ATP-DEPENDENT DISASSEMBLY OF CLATHRIN-COATED VESICLES.
                                                                                                                                                           LATTER G.I., SCHWENDER B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EUKARYOTA; METAŽOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; ARTIODACTYLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1994 (REL. 28, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
HEAT SHOCK 70 KD PROTEIN 6 (HEAT SHOCK 70 KD PROTEIN B').
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEZEGURE F., VAIMAN M., CHARDON P.;
BIOCHIM. BIOPHYS. ACTA 1174:17-26(1993).
-! INDUCTION: BY HEAT SHOCK.
-! SIMILARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
-1- SIMILARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HEAT SHOCK; ATP-BINDING; MULTIGENE FAMILY; ACETYLATION
                                       SLATER M.R.;
SUBMITTED (JUN-1993) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 84; DB 5; L
Pred. No. 6.89e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        260 rtacerakrtlsssaqtsveidslfegidfytsitrar 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 ROECGKPALPSASEEQVAQDMEG-FSAATFFTTISRNR 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 1 ACETYLATION.
641 AA; 69526 MW; 5B23162E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             643 AA
                                                                                                                                                     GARRELS J.I., FUTCHER B., KOBAYASHI R., VOLPE T., WARNER J.R., MCLAUGHLIN C.S.; ELECTROPHORESIS 15:1466-1486(1994).
                                                                                                                                                                                                                                 SEQUENCE OF 186-195.
STRAIN-ATCC 38531 / Y41;
NORBECK J., BLOMBERG A.;
FEMS MICROBIOL. LETT. 137:1-8(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL: X12926; G312352; -.
EMBL: L22015; G349747; ALT_SEQ-
PIR; S25438; HHBYAL:
PIR; S42164; S42164.
                       REVISIONS TO 207; 417 AND 421.
                                                                                               SEQUENCE OF 91-97 AND 325-341 STRAIN-$288C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P19120; 1NGJ.
SWISS-2DPAGE; P10591; YEAST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IEPD; 9788; ...
LISTA: SCO1202; SSA1.
SGD; L0002069; SSA1.
PROSITE; PS00297; HSP70_1.
PROSITE; PS00329; HSP70_2.
PROSITE; PS01036; HSP70_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 13.1%;
Best Local Similarity 26.3%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUE-LYMPHOCYTES;
MEDLINE; 93326632.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUS SCROFA (PIG).
                                                                                                                                     MEDLINE; 95203288
                                                                                                                                                                                                                                                                                                                                     ACETYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INIT_MET
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LT 9
HS76_PIG
Q04967;
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                                                                                       EDDY R.J., SAUTERER R.A., CONDEELIS J.S.;
EDDY R.J., SAUTERER R.A., CONDEELIS J.S.;
L. J. BIOL. CHEM. 268:23267-23274(1993).
I. J. BIOL. CHEM. 268:23267-23274(1993).
I. J. BIOL. CHEM. 268:2367-23274(1993).
I. THE ACTIN-BINDING PROTIEN CAPASZ/34. ACTS AS A CHAPERONE BY STIMULATING THE REFOLDING OF DENATURATED CAP32 AND CAP34.
I. SHELLING LOCATION: CYTOPLASMIC. FOOND IN F-ACTIN-RICH REGIONS OF THE CELL CORTEX AND CELL PROTRUCIONS.
I. SHECLIULARILY: BELONGS TO HEAT SHOCK COGNATE PROTEINS ARE EXPRESSED CONSTITUTIVELY DIRING NORMAL DEVELOPMENT.
I. SIMILLARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.
EMBL; X55739; G4133180; -.
BREAL; X55739; G433180; -.
BREAL; S65739; G433180; -.
BREAL; S65739; RSP70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MSSIGIDLGTTYSCVGVWQNDRVEIIAND -> IHHHINGNATWVVESGPVSEVLSFN (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-2388C / AB972;
MEDLINE; 9502812:
CLARK WH., KENG T., STORMS R.K., ZHONG W., FORTIN N., ZENG B.,
DELANK MS., OUBLLETTE B.F.F., BARTON A.B., KABACK D.B., BUSSEY H.;
                                       SEQUENCE FROM N.A., AND SEQUENCE OF 34-46; 102-106 AND 298-309.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 84; DB 5; Length 640;
Pred. No. 6.89e-01;
12; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0TU-1989 (REL. 11, CREATED)
01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
01-CCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
SASION YALOUSC.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N -> T (IN REF. 2)

N -> A (IN REF. 2)

S -> A (IN REF. 2)

V -> A (IN REF. 2)

V -> A (IN REF. 2)

V -> A (IN REF. 2)

F -> P (IN REF. 2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      641 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 590-641 FROM N.A.
MEDLINE; 89087943.
DOEDR N.C., LEE M.-C., KNAPP G.;
NUCLEIC ACIDS RES. 12:9367-9382(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 89128457.
SLATER M.R., CRAIG E.A.;
NUCLEIC ACIDS RES. 17:805-806(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              237
240
341
352
70499 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 13.1%;
Local Similarity 26.3%;
les 10; Conservative
EMBO J. 12:3763-3771(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PSO0329; HSP7C
PROSITE; PS01036; HSP7C
ATP-BINDING; CHAPERONE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240
341
352
352
3640 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                             MEDLINE; 94043116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LT 8
HS71_YEAST
P10591;
                                                           STRAIN-AX3
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CONFLICT
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SEQUENCE
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Matches

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Gaps

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Indels

Length 641;

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HSSP; P19120; 1NGJ.
PROSITE; PS00297; HSP70_1.
PROSITE; PS00329; HSP70_2.
PROSITE; PS01036; HSP70_3.
ATP-BINDING; HBAT SHOCK.
SEQUENCE 655 AA; 72051 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAT. GENET. 3:137-145(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 30.6%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=T-CELL;
MEDLINE; 90192810.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          UMBELLIFERAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LT 13
BAT2_HUMAN
P48634;
                                                                                                                                                                                                                                                                                          HS70_DAUCA
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                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                            / Match 13.1%; Score 84; DB 5; Length 643; Local Similarity 26.3%; Pred. No. 6.89e-01; nes 10; Conservative 12; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EUKARYOTA; FUNGI; MASTIGOMYCOTINA; CHYTRIDIOMYCETES.
EMBL; X68213; G1978; -.
PIR; S25585; S25585.
PIR; S34625; S34625.
HSSP; P19120; 1NGI.
PROSITE; P80029; HSP70_1.
R PROSITE; P801036; HSP70_2.
R PROSITE; P801036; HSP70_3.
ATP-BINDING; HEAT SHOCK; MULTIGENE FAMILY.
ATP-BINDING; HEAT SHOCK; MULTIGENE FAMILY.
                                                                                                                                                                                                                                                                     266 rtacerakrtlssstgatleidslfegvdfytsitrar 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           265 rtacdrakrtlssssgasieidslfegidfytaitrar 302
                                                                                                                                                                                                                                                                                          21-JUL 1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
ATAT SHOCK 70 KD PROTEIN (HSP70).
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
101-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
HEAT SHOCK 70 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                   647 AA.
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                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 81-120 FROM N.A. MEDLINE; 84221917.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE; 85076567.
BIENZ M.;
EMBO J. 3:2477-2483(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE; 95129910.
STEFANI R.M., GOMES S.L.;
GENE 152:19-26(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BLASTOCLADIELLA EMERSONII
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                                                                                                                                                                                                                                                                                                                                             10
HS70_XENLA
P02827;
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P48720;
                                                                                                                                                                                              Query Match
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Matches
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EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERWAE; DICOTYLEDONEAE; APIALES;
                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-1860 FROM N.A.
MEDLINE; 93272029.
IRIS F.J.M., BOUGUELERET L., PRIEUR S., CATERINA D., PRIMAS G.,
PERROT V., JURKA J., RODRIGUEZ-TOME P., CLAVERIE J.-M., DAUSSET J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                               ï
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                                                                                                                                    Query Match 13.1%; Score 84; DB 5; Length 649; Best Local Similarity 26.3%; Pred. No. 6.89e-01; Matches 10; Conservative 12; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 84; DB 5; Length 655;
Pred. No. 6.89e-01;
14; Mismatches 9; Indels
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MEDLINE; 92032789.
LIN X., CHERN M., ZIMMERMAN J.L.;
PLANT MOL. BIOL. 17:1245-1249(1991).
-! SIMILARIY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.
EMBL; X60088; G18357; -.
PIR; S18349; S18349.
-i- SIMILARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY. EMBL.; 122497; G773470; -. ATP-BINDING; CHAPENONE. SEQUENCE 649 AA; 70833 MW; 8ACFF56F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BANERJI J., SANDS J., STROMINGER J.L., SPIES T.;
PROC. NATL. ACAD. SCI. U.S.A. 87:2374-2378(1990)
                                                                                                                                                                                                                                               267 rtacerakrtlsssaqtsleidslfegidfytsitrar 304
                                                                                                                                                                                                                                                                           72051 MW; 791B240F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1992 (REL. 23, CREATED)
01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
01-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE)
HEAT SHOCK 70 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                               655 AA.
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PUTATIVE ROLE AS TRANSCRIPTION FACTOR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                        -1- TISSUE SPECIFICITY: LIMITED TO CELL-LINES OF LEUKAEMIC ORIGIN. BMBL; M33509; G179339; -. BMBL; M33518; G179345; -. BMBL; M33512; G179345; -. BMBL; M33512; G179345; -. BMBL; Z15025; G29375; -.
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4 X 57 AA TYPE A REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2-2.
3 X 50 AA TYPE C REPEATS.
3-1.
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Q06003;

Q1-FEB-1994 (REL. 28, CREATED)

Q1-FEB-1995 (REL. 28, LAST SEQUENCE UPDATE)

Q1-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)

GOLIATH PROTEIN (G1 PROTEIN).

GOLO R G1 OR G1.

DROSOPHILA MELANGASTER (FRUIT FLY).

EUKARYOTA; METAZOA; ARTHROPODA; INSECTA; DIPTERA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1-4.
2 X TYPE B REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2CFEF88A CRC32
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Pred. No. 6.89e-01;
                                                                                                                                                                                                                                                                                      GLN-RICH.
POLY-PRO.
POLY-PRO.
POLY-PRO.
POLY-PRO.
POLY-GLY.
POLY-GLY.
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Best Local Similarity 27.8%;
Matches 15; Conservative
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BOUCHARD M.L., COTE S.;
GENE 125:205-209(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2089
1948
2014
2089
                                                                        EMBL; M33518; G179345
EMBL; M33512; G179345
EMBL; 215025; G29375;
PIR; 235098; B35098.
PIR; 236152; S36152
MIM; 142580;
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1285
1400
1611
1729
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CON
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-I- FUNCTION: ALPHA-L-FUCOSIDASE IS RESPONSIBLE FOR HYDROLYSING THE ALPHA-1,6-LINKED FUCOSE JOINED TO THE REDUCING-END

N-ACETYLGLUCOSAMINE OF THE CARBOHYDRATE MOIETIES OF GLYCOPROTEINS.

-I- CATALYTIC ACTIVITY: AN ALPHA-L-FUCOSIDE + H(2)0 - AN ALCOHOL +
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                  273
                                                                                                                                                                                                                                                                             ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND SEQUENCE OF 29-40; 90-124 AND 307-372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ñ
                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1990 (REL. 15, CREATED)
01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
ALPHA-L-FUCOSIDASE PRECURSOR (EC 3.2.1.51) (ALPHA-L-FUCOSIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- SUBUNIT: HOMOTETRAMER.
-1- SUBCELLULAR LOCATION: LYSOSOMAL.
-1- SIMILARITY: BELONGS TO FAMILY 29 OF GLYCOSYL HYDROLASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALPHA-L-FUCOSIDASE.
MAY BE IMPORTANT FOR CATALYSIS.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                           Score 83; DB 4; Length 284;
Pred. No. 9.52e-01;
16; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 83; DB 4; Length 462;
Pred. No. 9.52e-01;
5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00385; ALPHA_L_FUCOSIDASE.
HYDROLASE; GLYCOSIDASE; LYSOSOME; GLYCOPROTEIN; SIGNAL.
SIGNAL
1 28
                                                                                                                                                        208 259 GLN/PRO/SER-RICH.
284 AA; 31973 MW; FB98BE96 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
4923CBE4 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                      462 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: Wed Aug 20 11:10:10 1997
Job time : 16 secs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                280 rphslpdhkwemctsvdkaswgyrrd 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 90147522.
FISHER K.J., ARONSON N.N. JR.;
BIOCHEM. J. 264:695-701(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53486 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 12.9%;
Best Local Similarity 46.2%;
Matches 12; Conservative
                                                                                                                                                                                                         Query Match
Best Local Similarity 26.3%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      462
292
237
264
378
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PIR; S07074; S07074.
PIR; S10235; S10235.
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DOMAIN
SEQUENCE
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FUCO_RAT
P17164;
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U.K. Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm Wed Aug 20 11:12:02 1997; MasPar time 5.48 Seconds 438.125 Million cell updates/sec MPsrch\_pp Run on:

Tabular output not generated.

Perfect Score: Description:

>US-08-320-157-22 (1-210) from US08320157.pep 1554

1 MASGOGPGPPRQECGEPALP.....LVVLGVVLLGQFVVRRFFKS 210 PAM 150 Scoring table: Seguence:

96640 seqs, 11439865 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

l:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 a-geneseq27 Database:

Variance 141.622; scale 0.229 Mean 32.457; Statistics:

No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, derived by analysis of the total score distribution. score g Pred.

### SUMMARIES

Result No.	Score	Query Match	Length DB	DB	OI OI	Description	Pred. No.
П	1543	99.3	211	20	W03668	Bak protein.	4.01e-136
8	1543	99.3	211	17	R81451	Bcl-Y apoptosis-relat	4.01e-136
m	1543	99.3	211	13	R77876		4.01e-136
4	1511	97.2	211	20	W03669	Bak-2 protein.	5.36e-133
'n	1511	97.2	211	13	R77877		5.36e-133
9	1136	73.1	152	13	R77879		1.82e-96
7	1061	68.3	141	13	R77880		3.42e-89
œ	880	9.99	116	13	R77881	Human Cdn-1(96-211).	1.07e-71
σ	258	16.6	190	13	R68884	Chicken lymphoid BCL-	3.49e-13
10	256	16.5	232	13	W01020	Apoptosis-blocking pr	5.25e-13
11	250	16.1	233	13	R68887	Human thymus BCL-XL.	1.79e-12
13	250	16.1	233	20	W05821	Bcl-XL protein.	1.79e-12
13	245	15.8	232	19	W01019	Apoptosis-blocking pr	4.95e-12
14	245	15.8	239	13	W01018	Apoptosis-blocking pr	4.95e-12
15	243	15.6	205	13	R71405	Human bcl-2 beta prot	7.43e-12
16	243	15.6	205	13	R68886	Human thymus BCL-2.	7.43e-12
17	243	15.6	205	13	R70332	Human bcl-2 protein.	7.43e-12
18	243	15.6	239	13	R71404	Human bcl-2 alpha pro	7.43e-12
19	243	15.6	239	6	R47344	Human oncodene bcl-2	7.43e-12
20	243	15.6	239	Н	P80987	Sequence of bcl-2-alp	7.43e-12

7.43e-12 7.43e-12 3.14e-09 3.14e-09 1.88e-08 1.36e-04 2.55e-06 6.50e-04 7.05e-00 1.36e-100 1.36e	3.64e+01 3.64e+01 3.64e+01 3.64e+01 4.27e+01 4.27e+01 4.27e+01 4.27e+01
Human bcl-2 protein. Bcl-2 oncogene produc Human cdn-3. Apoptosis-blocking pr Human Bax protein. Human Bax protein. Human mcl-1 gene prod Human thymus BCL-XI. Deduced sequence enco Human thymus BCL	Human mGluR4. Human mGluR4. Human type I inositol Human T cell inositol N. crassa mtr gene pr Mtr protein of Neuros Peripheral nervous sy Peripheral nervous sy
R70331 R42312 R42312 P607878 P60988 R71407 W01021 R71696 R68885 R76996 R68885 R76996 R73955 R13887 R73955 R73955 R73956 R73956 R73957 R73957 R73957	R82658 R72092 W07632 W00168 R79909 R47118 R99639
	912 14 912 13 2695 20 2713 19 451 14 470 9 1984 18
997711887878706777	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
244 24433 2013 2013 1004 1179 97 97 97 98	88 88 88 87 87 87
22222222222222222222222222222222222222	8000176448

#### ALIGNMENTS

protein

Disclosure; Fig 1: 24pp; English.

This Bak protein sequence represents a bcl-1 homologue which riteracts with Epstein-Bar virus (EBV) early lytic cycle BHRF1 interacts with Epstein-Bar virus (EBV) early lytic cycle BHRF1 protein, and is capable of modulating apoptosis. The protein may brotein, in a new virucide drug screening method, which involves combination of Bak protein and a viral protein (e.g. EBV BHRF1), exposure to a test compound, and monitoring for disruption of the interaction, e.g. by co-precipitation, protein interactive trapping or ELISA. Interaction of Bak and viral proteins allows viral ceplication or latency in the absence of apoptosis. Compounds which inhibit the interaction may be used as virucide, antitumour or Compounds which an antibody; Human; Bak; apoptosis; latency; virus replication; Epstein: Barr virus; BHRF1; fusion protein; epitope tag; drug screening; co-precipitation; ELISA; immunoassay; antibody; protein interactive trapping; virucide; antitumour; diagnostic. Screening for anti-viral agents - by detecting the ability of agent to disrupt the interaction of a Bak protein and a viral T 1 W03668 standard; Protein; 211 AA. 19-APR-1996; U05639. 20-APR-1995; US-426529. (LXRB-) LXR BIOTECHNOLOGY INC. 22-FEB-1997 (first entry) Barr PJ, Kiefer MC; WPI; 96-485886/48. diagnostic agents. Sequence 211 AA; N-PSDB; T42138. Homo sapiens Bak protein. 24-0CT-1996 Sequence RESULT 

Length 211; Indels Score 1543; DB 20; Pred. No. 4.01e-136; 0; Mismatches 0; 99.3%; larity 99.5%; Conservative Query Match Best Local Similarity Matches 210; Conser

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Query Match 99.3%;
Best Local Similarity 99.5%;
Matches 210; Conservative
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21-NOV-1995 (first entry)
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WPI; 96-485886/48.
                                                                                                                                                                                                                                                                            Barr PJ, Kiefer MC;
WPI; 95-215106/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bak-2 protein.
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                                                                                                                                                                                                                                                                                                                         N-PSDB; Q95492
                                                                                                                  Homo sapiens.
                       Human Cdn-1.
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N-PSDB; T17375.
New isolated human Bcl-Y protein - used to develop prods. for
troating disorders characterised by inappropriate cell proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 masgagpppraecgepalpsaseegvaddteevfrsyvfyrhqqeqeaegvaapadpem 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Fig 4: 100pp; English.

Bcl-Y protein (R81451) is a member of the Bcl-2 family and can induce apoptosis in cells and function as a negative regulator of Bcl-2 function. Bcl-Y mRNA was detected in all human tumour cell lines examined and is also widely expressed in primary human tissues. It can be obtd. by expression of a full-length cDNA clone (T1735) in pref. mammalian host cells. Bcl-Y can be used to develop prods. for treating disorders associated with inappropriate cell proliferation or cell death, and to raise antibodies used for the diagnosis or monitoring of such disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                       Query Match 99.3%; Score 1543; DB 17; Length 211; Best Local Similarity 99.5%; Pred. No. 4.01e-136; Matches 210; Conservative 0; Mismatches 0; Indels 1;
                                                                                                                                                                                                                                                                                                                                          R01451;
02-JUL-1996 (first entry)
Bcl-Y apoptosis-related protein.
Bcl-Y, apoptosis; cell proliferation; cell death; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Domain
/label- C-terminal_domain
/note- "putative membrane localisation sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 lnlgngpilnvlvvlgvvllggfvvrrffks 211
                                                                                                                                                                                                         180 LNLGNGPILNVLVVLGVVLLGQFVVRRFFKS 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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ID R77876 standard, Protein, 211 AA.
AC R77876,
                                                                                                                                                                                                                                                                                               T 2
R81451 standard; Protein; 211 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-FEB-1996.
09-AUG-1995; U10103.
09-AUG-1994; US-287427.
11-OCT-1994; US-321071.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (IMMU-) IMMUNOGEN INC. Chittenden TD;
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61 vtlplqpsstmgqvgrqlai1gddinrrydsefqtmlqhlqptaenayeyftkiatslfe 120
                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid sequences encoding cdn apoptosis modulators - and related vectors, transformed cells, proteins and antibodies, useful or diagnosis and treatment e.g. of HIV infection, reperfusion injury
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig. 3A-B; 66pp; English.

Cdn-1 cDNA was isolated from a human heart cDNA library using a previously isolated clone as probe. Recombinant Cdn-1 was produced in Sf9 and human colon adenocarcinoma HT29 cells. Expression of cdn-1 in WT-L2 lymphoblastoid cells resulted in increased cell survival in response to anti-Fas-mediated apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 1; Gaps
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This Bak-2 protein sequence represents a bcl-1 homologue which interacts with Epstein-Barr virus (EBV) early lytic cycle BHRF1 protein, and is capable of modulating apoptosis. The protein may
Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV autoimmune disease; reperfusion injury; hepatitis, osteoporosis; shock; lymphoma; eczema.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; Bax-2; apoptosis; latency; virus replication;
Epstein-Barr virus; BHRF1; fusion protein; epitope tag;
drug screening; co-precipitation; ELISA; immunoassay; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein interactive trapping; virucide; antitumour; diagnostic.
Homo sapiens.
WO9633416-A1.
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Pred. No. 4.01e-136;
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20-APR-1995; US-426529.
(LXRB-) LXR BIOTECHNOLOGY INC.
                                                                                                                                                                                                         30-NOV-1994; U13930.
30-NOV-1993; US-160067.
07-OCT-1994; US-320157.
(LXRB-) LXR BJOTECHNOLOGY INC.
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WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 vtlplqpsstmgqvgrqlaiigddinrrydsefqtmlqhlqptaenayeyftkiasslfe 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sginwgrvvallgfsyrlalhiygrgltgflggvtrfvvdfmlhhciarwiagrggwvaa 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           be used in complete or partial form, or as an epitope tag fusion protein, in a new virucide drug screening method, which involves combination of Bak-2 protein and a viral protein (e.g. EBV BRFEI), exposure to a test compound, and monitoring for disruption of the interaction, e.g. by co-precipitation, protein interactive trapping or ELISA. Interaction of Bak-2 and viral proteins allows viral replication or latency in the absence of apoptosis. Compounds which inhibit the interaction may be used as virucide, antitumour or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vtlplqpsstmgqvgrqlaiigddinrrydsefqtmlqhlqptaenayeyftkiasslfe 120
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                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cdn-2; apoptosis modulator; adoptive immunotherapy; therapy; HIV;
autoimmune disease; reperfusion injury; hepatitis, osteoporosis;
shock; lymphoma; eczema.
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Disclosure: Fig.5D-E; 66pp; English.
Cdn-2 cDNA was isold. from a human placental genomic library
using a 950 bp fragment of Cdn-1 cDNA. Expression of Cdn-2
in mouse progenitor B-cell Fi5.12 cells decreased IL-3-induced
apptosis. The Cdn-2 protein displayed 97% amino acid identity
with Cdn-1 (R77876).
Sequence 211 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
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                                                                                                                                                                                                                                                                                                                                                       Length 211;
                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                    97.2%; Score 1511; DB 20; 96.7%; Pred. No. 5.36e-133;
                                                                                                                                                                                                                                                                                                                                                                                                                 5; Mismatches
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30-NOV-1994; U13930.
30-NOV-1993; US-160067.
07-OCT-1994; US-320157.
(LXRB-) LXR BIOTECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97.2%;
96.7%;
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Best Local Similarity 96.7%;
Matches 204; Conservative
                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 96.7%;
les 204; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Barr PJ, Kiefer MC;
WPI; 95-215106/28.
N-PSDB; Q95493.
                                                                                                                                                                                                                                                      diagnostic agents
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WO9515084-A.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig.11; 66pp; English.

Expression of Cdn-1 in WI-L2 lymphoblastoid cells resulted in increased cell survival in response to anti-Fas-mediated apoptosis. Deletion of the N-terminal 59 amino acids of Cdn-1 only slightly decreased this activity, suggesting that small, truncated Cdn-1 Sequence 152 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 mvtlplqpsstmgqvgrqlai1gddinrrydsefqtmlqhlqptaenayeyftkiatslf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cdn-1; apoptosis andulator; adoptive immunotherapy; therapy; HIV, autoimmune disease; reperfusion injury; hepatitis, osteoporosis; shock; lymphoma; eczema.
                                                                                                                                                                                                                                                                                                    Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV autoimmune disease; reperfusion injury; hepatitis, osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid sequences encoding Cdn apoptosis modulators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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Pred. No. 1.82e-96;
0; Mismatches 0;
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                                                                                     181 Inlgngpilnvlvvlgvvllggfvvrrffks 211
                                                                                                              180 LNLGNGPILNVLVVIGVVLLGQFVVRRFFKS
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W09515084-A.

08-JUN-1995.

30-NOV-1994; U13930.

30-NOV-1993; US-160067.

07-0CT-1994; US-320157.

(LXRB-) LXR BIOTECHNOLOGY INC.
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30-NOV-1994; UJ3930.
30-NOV-1993; US-160067.
07-OCT-1994; US-320157.
(LXRB-) LXR BIOTECHNOLOGY INC.
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R77880;
                                                                                                                                                                                                                     standard; Protein; 152
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Best Local Similarity 99.3%;
Matches 151; Conservative
                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                     shock; lymphoma; eczema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kiefer MC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PJ, Kiefer MC;
95-215106/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human Cdn-1(71-211)
                                                                                                                                                                                                                                                                                  Human Cdn-1(60-211)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Barr PJ, Kiefer MC WPI; 95-215106/28.
                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
WO9515084-A.
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US-08-320-157-22.rag

Best Local Matches

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Boise LH, Numez G, Thompson CB,
WPI: 95-062079/07.
N-PSDB; 081696.
New POLY-nucleotide encoding new Poly-peptide(s) that modify
N-PSDB; 081696.
New Poly-nucleotide encoding new Poly-peptide(s) that modify
apoptosis - and related vectors, recombinant cells and
antibodies, useful in assay and for control of cell death in e.g.
neuronal cells, lymphocytes and cancers
claim 4; page 87: 127pp; English.
This protein may be expressed recombinantly, particularly with pcmV
plasmids as vectors for expression in mammalian cell cultures.
The protein has particular application in cancer cells (failure of
programmed cell death (PCD) or neurodegenerative and autoimmune diseases
(premature PCD), e.g. Parkinson's disease, amylotrophic lateral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 vvngatvhrsslevheivrasdvrgalrdagdefelryrrafsdltsglhitpgtaygsf 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 eqvvnelfhdgvnwgrivaffsfggalcvesvdkemrvlvgrivswmttyltdh-ldpwi 178
                                               Chicken lymphoid BCL-X.
Chicken; bird; fowl; BCL-X; apoptosis; cell death; cancer;
neurodegenerative disease; autoimmune disease; Parkinson's disease;
amylotrophic lateral sclerosis; multiple sclerosis; oncogene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WELF. 96-427055/43.

Nucleic acids encoding apoptosis regulating proteins - useful for diagnosing and treating immune disorders, malignancies, etc.
diagnosing and treating immune disorders, malignancies, etc.
Example 8; Page 34-35; 60pp; English.

Example 8; Page 34-35; 60pp; English.

The 80-6 mutant (W01020) of the bcl-2 oncogene product (W01018) lacks amino acids 80-86 of the native protein. This and other Bcl-2 mutants (see also W01019-21) were used in a two hybrid assay to examine the interactions between Bcl-2 and novel apoptosis-regulating proteins N1p1, N1p2 and N1p3 (W00997-99). 2 Motifs (W01003-04) on Bcl-2 were identified that are essential for interaction with the N1p proteins. These motifs show homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Apoptosis blocking protein Bcl-2 mutant 80-6 (del80-86). Apoptosis-regulating protein; Bcl-2; oncogene; adenovirus ElB 19K protein; cell death; cancer; tumour; immune disorder; dlagnosis; therapy; BiplA; Bipl3; Bip5; NIp1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 13; Length 190;
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Pred. No. 3.49e-13;
32; Mismatches 59
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W01020;
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28.2%;
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                                 entry)
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les 37; Conservative
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21-MAR-1996; 104542.
21-MAR-1995; US-408095.
(UYSL-) UNIV ST LOUIS.
                                                                                                                                                                                                           22-JUN-1994; U07089.
22-JUN-1993; US-081448.
(ARCH-) ARCH DEV CORP.
(UNMI ) UNIV MICHIGAN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            190 AA;
                                                                                                                                             Gallus domesticus.
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                                                                                                                                                                WO9500642-A.
                              10-AUG-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71 MGQVGRQLAIIGDDINRRYDSEFQIMLQHLQPIAENAYEYFTKIAISLFESG-NWGRVVA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ligfgyrlalhvyghgltgflggvtrfvvdfmlhhciarwiagrggwvaalnlgngpiln 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 mgqvgrqlaiigddinrrydsefqtmlqhlqptaenayeyftkiatslfesginwgrvva 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 mlqhlqptaenayeyftkiatslfesginwgrvvallgfgyrlalhvyqhgltgflgqvt 60
New nucleic acid sequences encoding Cdn apoptosis modulators - and related vectors, transformed cells, proteins and antibodies, useful or diagnosis and treatment e.g. of HIV infection, reperfusion injury
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid sequences encoding cdn apoptosis modulators - and related vectors, transformed cells, proteins and antibodies, useful or diagnosis and treatment e.g. of HIV infection, reperfusion injury
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                                                                                                                                                                                                                                                                                                                          Indels 1; Gaps
                                                                                     Disclosure; Fig.11; 66pp; English.

Expression of Cdn-1 in WI-L2 lymphoblastoid cells resulted in increased cell survival in response to anti-Fas-mediated apoptosis. Deletion of the N-terminal 70 amino acids of Cdn-1 improved this activity, suggesting that small, truncated Cdn-1 molecules may be potent therapeutics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig.11; 66pp; English.

Expression of Cdn-1 in WI-L2 lymphoblastoid cells resulted in Expression of Cdn-1 in WI-L2 lymphoblastoid cells resulted in Tesponse to anti-Fas-mediated apoptosis. Truncated Cdn-1 derivatives given in R77879-81 were used to test the effects of deleting the N-terminal sequences of Cdn-1 on this activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 rfvvdfmlhhctarwiaqrggwvaalnlgngpilnvlvvlgvvllgqfvvrrffks 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV; autoimmune disease; reperfusion injury; hepatitis, osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ï
                                                                                                                                                                                                                                                                               Length 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                          Score 1061; DB 13;
Pred. No. 3.42e-89;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 880; DB 13; L
Pred. No. 1.07e-71;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T. 8
R77881 standard; Protein; 116 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
ID R68884 standard; Protein; 190 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               190 VLVVLGVVLLGQFVVRRFFKS 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 vlvvlgvvllgqfvvrrffks 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-NOV-1993; US-160067.
07-OCT-1994; US-320157.
(LXRB-) LXR BIOTECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 99.1%;
Matches 115; Conservative
                                                                                                                                                                                                                                                                          / Match 68.3%;
Local Similarity 99.3%;
nes 140; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-NOV-1995 (first entry)
Human Cdn-1(96-211).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              shock; lymphoma; eczema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barr PJ, Kiefer MC;
WPI; 95-215106/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-NOV-1994; U13930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 AA;
                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence
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Indels

Query Match

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Best Loca Matches

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Inducing or preventing death of T cells by bcl-XL protein regulation used to increase survival of HIV infected cells or to dwn:regulate immune responses in immune diseases

Disclosure; Page 52-53; 76pp; English.

This is the sequence of a human bcl-XL protein, which protects
This is the sequence of a human bcl-XL protein, which protects
acks a stretch of 63 amino acids, and is a dominant negative
lacks a stretch of 63 amino acids, and is a dominant negative
regulator of bcl-XL function. The gene may be modified to
facilitate interaction with costimulatory Bax protein and inhibit
interaction with antagonistic Bad protein, by modification of the
Bcl-2 homology domains BHI and/or BHZ. The bcl-XL gene may be
introduced into T-cells in vivo or ex vivo via gene transfer using
a vector for HIV infection gene therapy, to augment intracellular
continuous protein levels and protect from cell death. A corresponding
antisense oligonuclectide or expression vector may be used in gene
therapy of e.g. autoimmune disease, graft rejection or graft.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 dspavngatghs-ssldarevipmaavkqalreagdefelryrrafsdltsqlhitpgta 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 yqsfeqvvnelfrdgvnwgrivaffsfggalcvesvdkemqvlvsriaawmatylndh-l 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48 EAEGVAAPADPEMVTLPLQPSSTMGQVGRQLAIIGDDINRRYDSEFQTMLQHLQPTAENA 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Apoptosis-blocking protein Bcl-2 mutant 42-8 (del42-48). Apoptosis-regulating protein; Bcl-2; oncogene; adenovirus ElB 19K protein; cell death; cancer; tumour; immune disorder; diagnosis; therapy; BiplA; BiplA; Bipl3; Bip5; NIp1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    down-regulate the immune response in a T-lymphocyte population
Bcl-XL protein.

Human; bcl-XL; T-lymphocyte; cell death; BH1 domain; BH2 doma
Bcl-2 homology domain; gene therapy; HIV; AIDS; antisense;
immune disorder; autoimmune disease; graft rejection;
graft-versus-host disease; apoptosis; adoptive immunotherapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16.1%; Score 250; DB 20; Length 233; 25.5%; Pred. No. 1.79e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41; Mismatches 60;
                                                                                                                             Location/Qualifiers
129..148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .T 13
W01019 standard; Protein; 232 AA.
W01019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 epwiqenggwdtfvelygnna 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   || : ||| : ::| || :
167 ARWIAQRGGWVAALNL-GNGP 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-DEC-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36; Conservative
                                                                                                                                                                                        180..191
                                                                                                                                                                                                                                                             02-MAY-1996,

02-MAY-1996, U06203,

04-MAY-1995, US-435518,

07-UNN-1995, US-481739,

(ARCH-) ARCH DEV CORP.

(USNA ) US SEC OF NAVY.

June CH, Thompson CB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-MAR-1995; US-408095. (UYSL-) UNIV ST LOUIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-MAR-1996; 104542.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                            /note= "BH2 domain"
                                                                                                                                                                     /note- "BH1 domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          233 AA;
                                                                                                                                                                                                                                                                                                                                                                                                       WPI: 96-506159/50.
                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; T40079
                                                                                                                                                                                                                              WO9634956-A1.
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                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nip2; Nip3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-SEP-1996
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Matches
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                                                                                                                             7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       optosis; cell death; cancer; neurodegenerative disease; disease; Parkinson disease; amylotrophic lateral sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48 ffssqpghtphp-aasrdpvartsplqtpaapgspvppvvhltlrqagddfsrryrrdfa 106
                                                                                                                                                                                                                                                61 dspavngatghs-ssldarevipmaavkgalreagdefelryrrafsdltsglhitpgta 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 yqsfeqvvnelfrdgvnwgrivaffsfggalcvesvdkemqvlvsriaawmatylndh-1 178
                                                                                                                                                                                                                                                                                         95 TMLOHLOPTAENAYEYFTKIATSLFESG-NWGRVVALLGFGYRLALHVYQHGLTGFLGQV 153
                                                                                                                                                                                             New Poly-nucleotide encoding new poly-peptide(s) that modify apoptosis - and related vectors, recombinant cells and antibodies, useful in assay and for control of cell death in e.g. neuronal cells, lymphocytes and cancers
Claim 3; Page 94; 127pp; English.
This protein may be expressed recombinantly, particularly with pcmV plasmids as vectors for expression in mammalian cell cultures, protein has particular application in cancer cells (failure of programmed cell death (PCD) or neurodegenerative and autoimmune diseases (premature PCD), e.g. Parkinson's disease, amylotrophic lateral sclerosis and multiple sclerosis.
                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Gaps
                                                                                                                             6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 250; DB 13; Length 233;
Pred. No. 1.79e-12;
41; Mismatches 60; Indels (
                                                                                     Length 232
to motifs (W01005-06) identified on the adenovirus ElB 19K
                                                                               Score 256; DB 19;
Pred. No. 5.25e-13;
40; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                167 alwmteylnrh-lhtwigdnggwdafvel-ygpsmrpl 202
                      apoptosis-blocking protein (W01010)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Boise LH, Nunez G, Thompson CB; WPI; 95-052079/07.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R68887 standard; Protein; 233 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BCL-XL; apoptosis; cell death;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 epwiqenggwdtfvelygnna 199
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16.1%;
Best Local Similarity 25.5%;
Matches 36; Conservative
                                                                               Match 16.5%;
Local Similarity 29.7%;
les 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAR-1997 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-JUN-1994; U07089.
22-JUN-1994; US-081448.
(ARCH-) ARCH DEV CORP.
(UNMI ) UNIV MICHIGAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human thymus BCL-XL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     multiple sclerosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
WO9500642-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          autoimmune
                                              Seguence
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W05821;

RESULT ID WO AC WO DT 30

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protein regulation

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Best Local Similarity
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        Query Match
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                              Nucleic acids encoding apoptosis regulating proteins - useful for diagnosing and treating immune disorders, malignancies, etc.

diagnosing and treating immune disorders, malignancies, etc.

Example 8; page 33-34; 60pp; English.

The 42-8 mutant (W01019) of the bcl-2 oncogene product (W01018)

Lacks amino acids 42-48 of the native protein. This and other

E Bcl-2 mutants (see also W01020-21) were used in a two hybrid assay

to examine the interactions between Bcl-2 and novel apoptosis-

regulating proteins Nipl, Nip2 and Nip3 (W00997-99). The Nip

C proteins were unable to interact with mutant 42-8. The site of

deletion in this mutant corresponds to a motif (see also W01003)

C binding motif (W01004) of Bcl-2 was also identified, and both

show homology to motifs (W01005-06) found on the 19K protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 tvvoelfrdgvnwgrivaffefggvmcvosvnremsplvdnialwmteylnrh-lhtwig 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The Sep-1996. 104442.

21-MAR-1996; 104442.

22-MAR-1996; 105-408095.

33 (UYSL-) UNIV ST LOUIS.

Chinadurai G;

WPI; 964427055/43.

The Chinadurai G;

WRI 996; 1056/42.

The Bod of treating immune disorders, malignancies, etc.

The bod of treating immune disorders, etc.

The bod of treating immune disorders is induced by the bod of the of the 19K

Protein (WOLOIO) of denovirus Elb. 3 Novel proteins, Bipla, and Bipla and Bipla (MOLOIO), that specifically interact with Bod MOLOID-21) shows the apoptosis-regulating Nip proteins (see also WOLOID-21) shows the apoptosis-regulating Nip proteins (see also MOLOID-21) and Bibla and 
                                                                                                                                                                                                                                                                                                                                                                                                                                  tpaapgaaagpalspvppvvhlt--lrqagddfsrryrrdfaemssglhltpftargcfa 124
                                                                                                                                                                                                                                                                                                                                                                                            6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Apoptosis-blocking protein Bcl-2, Apoptosis-regulating protein; Bcl-2; oncogene; adenovirus ElB 19K protein; cell death; cancer; tumour; immune disorder; diagnosis; therapy; Bipla; Bipl3; Bip5; NIP1;
                                                                                                                                                                                                                                                                                                                                                   Score 245; DB 19; Length 232;
Pred. No. 4.95e-12;
36; Mismatches 57; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label-Binding_motif
/note- "interacts with Bip proteins"
EP-733706-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Binding_site 43..51
/label~ Binding_motif
/note⇔ "interacts with Bip proteins"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W01018 standard; Protein; 239 AA.
W01018;
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172 QRGGWVAALNLGNGPILNVL 191
                                                                                                                                                                                                                                                                                                                                                   15.8%;
Local Similarity 29.3%;
les 41; Conservative
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Chinnadurai G;
WPI; 96-427055/43.
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                                                                                                                                                                                                                                                                                                                                                     Query Match
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Wethods for producing and identifying mutant bol-2 proteins -
that lack death repressor activity and/or lacks binding to Bax.

By Disclosure; Bage 40; 1379p; Banglish.

The sequences given in R71404-05 represent the human bol-2 alpha and
beta proteins respectively. bol-2 is encoded by a proto-oncogene and
construction by enhancing apoptosis in many hematopoietic cells systems.
bol-2 is a 26 kD membrane-associated cytoplasmic protein and is thought
co function by enhancing the survival of hematopoietic cells of B and T
corigins rather than directly promoting proliferation of these cell
cycle
corigins rather than directly promoting proliferation of these cell
cycle
corigins rather than directly promote cell cycle
corigins rather than directly promote cell cycle
corigins rather than directly promote cell cell coll ben shown to directly promote cell cell coll
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concentrations of IL-3. bol-2 has been shown to form hererodiners with
concentrations of IL-3. bol-2 has been shown to form hererodiners with
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concentrations of IL-3. bol-2 has been shown to form hererodiners with
concentrations of IL-3. bol-2 has been shown to form hererodiners with
concentrations of IL-3. bol-2 has been shown to form here connect the death repressor activity of bol-2 in which there is at least one amino acid substitution or deletion
in the BHI or BH2 domains. This makes the mutant protein substantially
concentring death effector molecules. Up regulating bol-21s beneficial in
treatment and diagnosis of immunodeficiency diseases, including AIDS and
concrament and diagnosis of immunodeficiency diseases, including AIDS and
concrament and allament cell death.
Sequence 205 Ax;
                                                                                                                                                                                                    132 tvveelfrdgvnwgrivaffefggvmcvesvnremsplvdnialwmteylnrh-lhtwig 190
                                                                                                                                                    74 tpaapgaaagpalspvppvvhlt--lrqagddfsrryrrdfaemssglhltpftargcfa 131
                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human bel-2 beta protein.

Human; bel-2; alpha; beta; proto-oncogene; hematopoietic cell line;

Human; bel-2; alpha; beta; proto-oncogene; hematopoietic cell line;

apoptosis; membrane-associated cytoplasmic protein; B cell; T cell;

proliferation; cell cycle progression; Bax; apoptotic cell death;

apoptosis; cytokine; death repressor; BH1; BH2; cancer therapy;

hyperplasia; immunodeficiency disease; AIDS; neurodegeneration;

ischaemic cell death.
                                                                                ;
0
    Length 239;
                                                                                Mismatches 57; Indels
                                    Pred. No. 4.95e-12;
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WO9505750-A.
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136..155
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                                                                                    36;
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172 QRGGWVAALNLGNGPILNVL 191
15.8%;
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                                                                                41; Conservative
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26-AUG-1993; US-112
                            Best_Local Similarity
Matches 41; Conser
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95-106605/14.
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Length 205;

Score 243; DB 13; Pred. No. 7.43e-12;

15.6%;

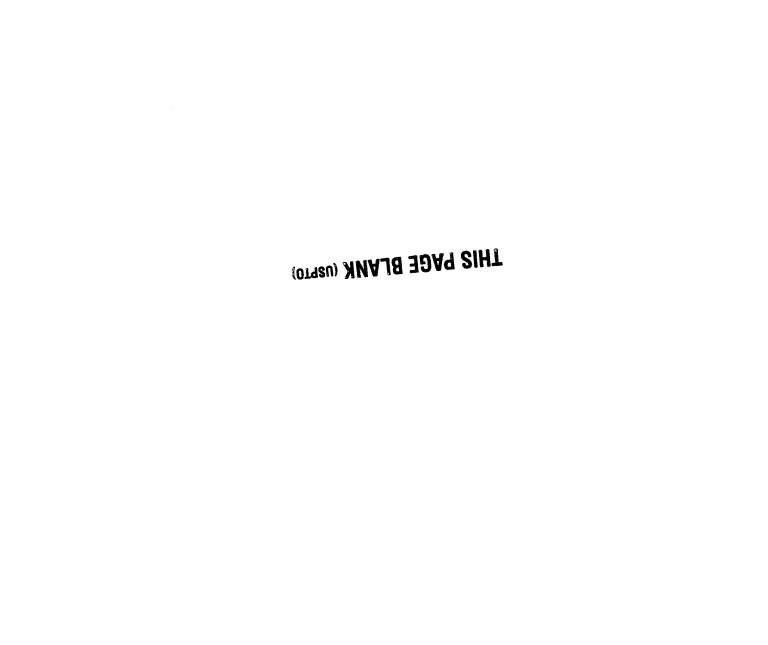
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Search completed: Wed Aug 20 11:12:27 1997 Job time : 25 secs.



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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Wed Aug 20 11:12:45 1997; MasPar time 9.69 Seconds 626.144 Million cell updates/sec Run on:

Tabular output not generated.

Title:

Description: Perfect Score: Sequence:

>US-08-320-157-22 (1-210) from USO8320157.pep 1554 1 MASGGCPGPPRQECGEPALP......LVVLGVVLLGQFVVRRFFKS 210

PAM 150 Gap 11 Scoring table:

91006 segs, 28888923 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

pir51
1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3
8:unann4 9:unann5 10:unann6 11:unann7 12:unann8
13:unann9 14:unann10 15:unenc 16:unrev

Mean 45.070; Variance 107.726; scale 0.418 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

			Q	,			_	_	_	_	_				_							
	Pred. No	1.46e-24	6.54e-236	6.91e-22	2.79e-21	2.79e-21	1.13e-20	3.19e-20	4.51e-20	6.38e-20	1.27e-19	5.07e-19	5.07e-19	1.42e-18	2.83e-18	2.83e-18	2.83e-18	7.90e-18	1.21e-16	5.11e-14	1.93e-12	9.88e-12
	Description	Bak protein - human	cdn-2 protein - huma	apoptosis requlator	BCL-X protein - rat	bcl-x long - mouse	apoptosis requlator	bcl-x transmembrane	transforming protein	transforming protein				BCL-X-Long - rat	transforming protein	transforming protein	transforming protein	BCL-2 - rat (fragmen	transforming protein	programmed cell deat	bcl-2-associated pro	bcl-2-associated pro
COLUMNICO	Ð	S58873	S58875	A47537	S51761	I49056	B47537	I49057	B37332	A37332	TVHUB1	D37332	TVHUA1	I67431	TVMSB1	TVMSA1	E37332	167432	S24390	D47538	A47538	B47538
	DB	13	13	13	14	14	13	14	9	9	~	φ	~	14	7	~	9	14	ø	14	13	13
	Query Match Length	211	211	190	233	233	233	214	216	233	202	206	239	233	199	236	237	236	232	192	192	218
	Query	9.3	7.2	9.9	6.3	6.3	6.1	6.6	5.8	15.8	5.6	5.4	15.4	5.2	5.1	5.1	5.1	4.9	14.4	3.2	2.5	2.5
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BCL2 homolog MCL1 - bax - rat (fragment) gene bcl-2 protein - BAX splice form delt hemopoletic-specific cytochrome-c oxidase gop protein - satell beta-glucosidase - S gene NXIO protein - coat protein - straw NR-13 protein - quain	phosphatidyl-N-methy bcl-x short - mouse threonine synthase ( metabotropic glutama myosin heavy chain-B collagen alpha 3(IV) glycoprotein D - hum human blood group an hypothetical protein dimethylaniline mono hypothetical protein acetylglutamate kina metabotropic glutama
A47476 155295 158194 138921 249449 S46949 GPBPP4 53958 54148689 S44178	B22443 149055 SYBSRA ISB149 B43402 A39024 I55608 A49640 A49640 B35182 S5681 S5681 S22389
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Nature (1995) 374:136-739
Modulation of apoptosis by the widely distributed Bcl-2
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apoptosis regulator bcl-x - chicken
#formal_name Gallus gallus #common_name chicken
03-May-1994 #sequence_revision 03-May-1994 #text_change
A47537
A47537
                                  Gaps
                                                                                                                                                                                                                                                                                                                                                       cdn-2 protein - human
#formal_name Homo sapiens #common_name man
15.Feb-1996 #sequence_revision 01-Mar-1996 #text_change
01-Mar-1996
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##cross-references EMBL:U16812
##noto the nucleotide sequence was submitted to the EMBL
##noto the nucleotide sequence was submitted to the EMBL
##noto the nucleotide sequence was submitted to the EMBL
##noto the nucleotide sequence was submitted to the EMBL
Library, November 1994
# length 211 #molecular-weight 23411 #checksum 9485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          preliminary; nucleic acid sequence not shown; translation not shown
    Length 211;
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Pred. No. 6.54e-236;
5; Mismatches 1;
   Score 1543; DB 13;
Pred. No. 1.46e-241;
0; Mismatches 0;
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sin - human
 99.3%;
larity 99.5%;
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S58875
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Local Similarity 96.7%;
168 204; Conservative
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Best Local Similarity
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 Bolse, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.;
Lindsten, T.; Turka, L.A.; Mao, X.; Nunez, G.; Thompson,
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                                     Cell (1993) 74:597-608
bcl-x, a bcl-2-related gene that functions as a dominant
regulator of apoptotic cell death.
A47537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #formal_name Rattus norvegicus #common_name Norway rat 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 01-Dec-1995
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#length 233 #molecular-weight 26130 #checksum 6378
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submitted to the EMBL Data Library, November 1994
$51762
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Pred. No. 6.91e-22;
32; Mismatches 59; Indels
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Best Local Similarity 25.5%; Pred. No. 2.79e-21;
Matches 36; Conservative 41; Mismatches 60; Indels
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X #hength 190 #molecular-weight 21467
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Best Local Similarity 28.2%;
Matches 37; Conservative
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Lindsten, T.; Turka, L.A.; Mao, X.; Nunez, G.; Thompson,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #authors Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.
#journal J. Immunol. (1994) 153:4388-4398
#title Cloning and molecular characterization of mouse bcl-x in and T lymphocytes.
#cross-references WUID:95052604
                                                                                                                                                                                                                                                                       ##residues 1-233 ##label RES ##cross-references EMBL:U10101; NID:g506647; CDS_PID:g506648 #WCE ##cross-references EMBL:U10101; NID:g506647; CDS_PID:g506648 #WCE #MCE Kamesaki, H.; Michaud, G.Y.; Takatsu, K.; Okuma, M. bmission submitted to the EMBL Data Library, November 1994 scription IL-5 inhibits anti-IgM-induced apoptosis in an immature icall line through inductin of bcl-X1.
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Pred. No. 2.79e-21;
41; Mismatches 60; Indels 4; Gaps
                 bcl-x long - mouse
#formal_name Mus musculus #common_name house mouse
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
15-Oct-1996
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#formal_name Homo sapiens #common_name man
16.Aug-1996 #sequence_revision 16-Aug-1996 #text_change
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##residues
##cross-references EMBL:X83574
X #length 233 #molecular-weight 26132 #checksum 5739
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apoptosis regulator bcl-xL - human
bcl-2-related protein
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##cross-references GB:L20121; CDS_PID:Q07817
cession C47537
#type complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #authors Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W. #journal J. Immunol. (1994) 153:4388-4398 #title Cloning and molecular characterization of mouse bcl-x in and T lymphocytes. #cross-references MUID:95052604
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##residues
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Local Similarity 25.5%; Pred. No. 1.13e-20;
nes 36; Conservative 41; Mismatches 60; Indels
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transforming protein (bcl-2-beta) - chicken
##molecule_type mRNA
##residues 1-69,'G',71-125,189-233 ##label BO2
##cross-references GB:L20122; CDS_PID:g623237
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#length 214 #molecular-weight 23900
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bcl-x transmembrane deleted - mouse
                                                                                                     ##cross-references GDB:228079
iDS alternative splicing; apoptosis
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                                                                                   GDB: BCL2L
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Nucleic Acids Res. (1992) 20:4187-4192
Isolation and characterization of the chicken bcl-2 gene:
expression in a variety of tissues including lymphoid and
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                                                                                          Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. (1992) 20:417-4192
Isolatrion and characterization of the chicken bcl-2 gene expression in a variety of tissues including lymphoid neuronal organs in adult and embryo.
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#formal_name Gallus gallus #common_name chicken 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change
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Pred. No. 4.51e-20;
37; Mismatches 56; Indels
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Pred. No. 6.38e-20;
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Best Local Similarity 28.5%;
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A37332; S35453
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#authors Tsujimoto, Y.; Croce, C.M.
#journal Proc. Natl. Acad. Sci. U.S.A. (1986) 83:5214-5218
Proc. Natl. Acad. Sci. U.S.A. (1986) 83:5214-5218
Analysis of the structure, transcripts, and protein products of bcl-2, the gene involved in human follicular lymphoma.
#cross-references MUID:86259760
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##cross-references GDB:119031
#map_position 18q21.33-18q21.33
CLASSIFICATION #superfamily bol transforming protein
Alternative splicing, B-cell lymphoma; follicular lymphoma;
transforming protein
transforming protein
#length 205 #molecular-weight 22182 #checksum 1183
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Nucleic Acids Res. (1992) 20:4187-4192
Isolation and characterization of the chicken bcl-2 gene:
expression in a variety of tissues including lymphoid are
neuronal organs in adult and embryo.
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                                                                                      TVHUB1 #type complete
transforming protein bcl-2-beta - human
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#Journal Proc. Natl. Acad. Sci. U.S.A. (1986) 83:5214-5218
#title Analysis of the structure, transcripts, and protein products
of bcl-2, the gene involved in human follicular lymphoma.
#accession A29409
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#journal EMBO J. (1988) 7:123-131
#title Alternative promoters and exons, somatic mutation and derequiation of the Bcl-2--Ig fusion gene in lymphoma.
#cross-references MUID:88196071
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this sequence has been corrected in reference A37332
S02452
54 APADPEMVTLP-LQPSSTMGQVGRQLAIIGDDINRRYDSEFQTMLQHLQPTAENAYEYFT 112
                                                             133 tvveelfrdgvnwgrivaffefggvmcvesvnremsplvdnialwmteylnrh-lhtwig 191
                                                                                              Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. (1992) 20:4187-4192
Isolation and characterization of the chicken bcl-2 gene:
expression in a variety of tissues including lymphoid a
neuronal organs in adult and embryo.
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#authors Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.
#journal Endocrinology (1995) 136.232-241
#title Expression of members of the bcl-2 gene family in the immature rat overy: equine chorionic gonadotropin-mediated inhibition of granulosa cell apoptosis is associated with decreased bax and constitutive bcl-2 and bcl-xlong messenger ribonucleic acid levels.
#accession 167431
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#superfamily bcl transforming protein
alternative splicing; B-cell lymphoma; follicular lymphoma;
proto-oncogene; transforming protein
#length 239 #molecular-weight 26266 #checksum 8323
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sidues 1-6,'S',8-58,'T',60-128,'C',130-239 ##label HUA2 the sequence was determined from the germine gene Constitutive expression of BCL2 following t(14:18) chromosomal translocation is typically found in follicular lymphoma.
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Pred. No. 1.42e-18;
30; Mismatches 50; Indels 3; Gaps
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transforming protein bcl-2-beta - mouse
#formal_name Mus musculus #common_name house mouse
31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #formal_name Rattus norvegicus #common_name Norway rat 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 26-Jul-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 239;
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Pred. No. 5.07e-19;
36; Mismatches 57;
                                                                                                                                                                                                                                                                                  ##cross-references GDB:119031
#map_position 18q21.33-18q21.33
FUNCTION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 15.4%;
Best Local Similarity 29.3%;
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Best Local Similarity 28.4%;
Matches 33; Conservative
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BCL-X-Long -
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#journal Cell (1987) 49:455-463
#iiilo Molecular analysis of mbcl-2: structure and expression of the murine gene homologous to the human gene involved in #cross-references MUID:87187643
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                                                                                                                                                                                                                                                                                                                                                                                                                             94 lrragddfsrryrrdfaemssqlhltpftargrfatvveelfrdgvnwgrivaffefggv 153
                                                    Negrini, M.; Silini, E.; Kozak, C.; Tsujimoto, Y.; Croce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A90893
Nogrini, M.; Silini, E.; Kozak, C.; Tsujimoto, Y.; Croce,
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                                                                                                                                                                                                                                                                                                                                                                            2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TVMSA1 *type complete
transforming protein bcl-2-alpha - mouse
*formal_name Mus musculus *common_name house mouse
31-bc-1988 *sequence_revision 31-bc-1988 *text_change
02-Jun-1994
                                                                       #journal Cell (1987) 49:455-463
#title Molecular analysis of mbcl-2: structure and expression murine gene homologous to the human gene involved in follicular lymphoma.
#cross-references wIID:87187643
#accossion B25960
                                                                                                                                                                                                                                                              ***superfamily bc! transforming protein alternative splicing; transforming protein #length 199 #molecular-weight 22299 #checksum 7397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       *Superfamily bcl transforming protein alternative splicing; transforming protein #length 236 *molecular-weight 26524 *checksum 6709
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Bost Local Similarity 30.4%; Pred. No. 2.83e-18;
Matches 35; Conservative 30; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                         Length 199;
                                                                                                                                                                                                                                                                                                                                     Score 234; DB 2; Length 199;
Pred. No. 2.83e-18;
28; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sourch completed: Wed Aug 20 11:13:22 1997 Job time : 37 secs.
                                                                                                                                                                                           ##molecule_type DNA
##residues 1-199 ##label NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##molecule_type DNA
##residues 1-236 ##label NEG
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Best Local Similarity 31.1%;
Matches 32; Conservative
02-Jun-1994
B25960
A90893
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CLASSIFICATION
KEYWORDS
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                ACCESSIONS
REFERENCE
#authors
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DATE
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Wed Aug 20 11:13:40 1997; MasPar time 6.35 Seconds 701.611 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-320-157-22 (1-210) from USO8320157.pep 1554 1 MASGOGPGPPRQECGEPALP......LVVLGVVLLGQFVVRRFFKS 210

Description: Perfect Score: Sequence: Title:

PAM 150 Gap 11 Scoring table:

59021 seqs, 21210388 residues Searched:

Post-processing:

Minimum Match 0% Listing first 45 summaries

swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 Database:

Mean 46.936; Variance 89.738; scale 0.523 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		æ					
Result No.	Score	Query Match	Length	DB	QI	Description	Pred. No.
-	258	16.6	190	7	BCLX_CHICK	APOPTOSIS REGULATOR B	1.75e-27
7	254	16.3	233	Н	BCLX_RAT	APOPTOSIS REGULATOR B	9.85e-27
ო	250	16.1	233	٦	BCLX_HUMAN	APOPTOSIS REGULATOR B	5.51e-26
4	245	15.8	233	Н	BCL2_CHICK	APOPTOSIS REGULATOR B	4.70e-25
Ŋ	239	15.4	205	П	BC2B_HUMAN	PROTEIN BCL-2-BETA.	6.08e-24
φ	239	15.4	239	٦	BC2A_HUMAN	PROTEIN BCL-2-ALPHA.	6.08e-24
7	234	15.1	199	Н	BC2B_MOUSE	PROTEIN BCL-2-BETA.	5.08e-23
œ	234	15.1	236	Н	BC2A_MOUSE	PROTEIN BCL-2 ALPHA.	5.08e-23
6	232	14.9	236	Н	BCL2_RAT	PROTEIN BCL-2 ALPHA.	1.18e-22
10	206	13.3	192	г	BAXA_MOUSE	APOPTOSIS REGULATOR B	5.98e-18
11	194	12.5	192	٦	BAXA_HUMAN	APOPTOSIS REGULATOR B	7.87e-16
12	189	12.2	218	П	BAXB_HUMAN	APOPTOSIS REGULATOR B	5.86e-15
13	176	11.3	350	φ	MCL1_HUMAN	INDUCED MYELOID LEUKE	1.00e-12
14	165	10.6	143	7	BAXD_HUMAN	BAX PROTEIN, CYTOPLAS	7.08e-11
15	158	10.2	172	S	HSA1_MOUSE	HEMOPOIETIC - SPECIFIC	1.01e-09
16	126	8.1	179	٣	EAR_ASFE4	APOPTOSIS REGULATOR B	1.00e-04
11	121	7.8		m	EAR_ASFB7	APOPTOSIS REGULATOR B	5.41e-04
18	118	7.6	179	m	EAR_ASFM2	APOPTOSIS REGULATOR B	1.46e-03
19	116	7.5	255	7	COX3_CAEEL	CYTOCHROME C OXIDASE	2.80e-03
20	107	6.9	626	S	HTPG_BACSU	HEAT SHOCK PROTEIN HT	4.87e-02
21	106	9.8	133	4	GOP_BPP4	GOP PROTEIN.	6.63e-02
22	86	6.3	206	7	PEM2 YEAST	METHYLENE-FATTY-ACYL-	7.26e-01

1. 29e+00 3. 01e+00 3. 01e+00 2. 28e+00 2. 28e+00 2. 28e+00 2. 28e+00 2. 28e+00 3. 02e+00 3. 02e+00 5. 23e+00 5. 23e+00 6. 87e+00 6. 87e+00 6. 87e+00 9. 00e+00 9. 00e+00 9. 00e+00 9. 00e+00
THREONINE SYNTHASE (E MYOSIN LIGHT CHAIN 1, HYPOTHETICAL 59.6 KD HYPOTHETICAL 59.6 KD HYPOTHETICAL 60.5 KD DIMETHYLANLINE MONOO HYPOTHETICAL 95.4 KD ARG11 PROTEIN PRECURS METABOTROPIC GLUTHANT HYPOTHETICAL 14,5-TRISPH MORPHINE 6-DEHYDROGEN DNA-DIRECTED RNA POLY 0X40L RECEPTOR PRECUR 43.2 KD PROTEIN IN HM HYPOTHETICAL 45.7 KD 3-PHOSPHOSHIKMATE 1-HYPOTHETICAL 45.7 KD HYPOTHETICAL 54.5 KD MINOR CAPSID PROTEIN (EGER RENDOGLUCANASE E PRECU
THRC_PSEAE MLEF_HUMAN YAC1_ECOLI YAC1_ECOLI YAC1_ECOLI YAC2_ECHO YP60_METTH FUG2_RABIT YAC3_RABIT YAC3_RABIT YAC3_RABIT YAC3_RABIT YAC4_HUMAN HUMC3_DESPH HUMC4_HUMAN HUMC3_DESPH YGG1_DESPH YGG1_DESP
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### ALIGNMENTS

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233 AA.

PRT;

STANDARD;

RESULT 2 ID BCLX\_RAT

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A MEDLINE; 93364977.
A BOISE L.H., GONZALEZ-GARCIA M., POSTEMA C.E., DING L.,
BOISE L.H., GONZALEZ-GARCIA M., POSTEMA C.E., DING L.,
L. LINDSTEN T., TURKA L.A., MAO X., NUNEZ G., THOMPSON C.B.;
CELL 74:597-608(1993).
C -!- FUNCITON: DOMINANT REGULATOR OF APOPTOTIC CELL DEATH.
C -!- FUNCITON: DOMINANT REGULATOR OF APOPTOTIC CELL DEATH.
C -!- TISSUES PERCIFICITY: BCL.X(S) IS EXPRESSED AT HIGH LEVELS IN CELLS
THAT UNDERGO A HIGH RATE OF TUNOVER, SUCH AS DEVELOPING
LUMPHOCYTES. IN CONTRAST, BCL.X(L) IS FOUND IN TISSUES CONTAINING
C LONG-LIVED POSTMITOTIC CELLS, SUCH AS ADULT BRAIN.
C -!- SIMILARITY: BELONGS TO THE BCL.2 FAMILY.
R EMBL; Z23115; G510901; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 yqsfeqvvnelfrdgvnwgrivaffsfggalcvesvdkemqvlvsriaswmatylndh-1 178
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MICHAELING 
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                                                                                                                                                                                                                                                      RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HOMO SAPIENS (HUMAN).
EUKARYOTA; METALOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 254; DB 1; Length 233;
Pred. No. 9.85e-27;
41; Mismatches 60; Indels
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G -> A (IN G510901).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126 188 MISSING (IN BCL-X(S)).
233 AA; 26130 MW; E0589815 CRC32;
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01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
                                       01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
APOPTOSIS REGULATOR BCL-X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     233 AA
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APOPTOSIS; ALTERNATYE SPLICING.
126 188 MIS
CONFLICT 70 G G G
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Best Local Similarity 25.5%;
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APOPTOSIS REGULATOR BCL-X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; 223116
EMBL; 223115
MIM; 600039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BCLX_HUMAN
Q07817;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDOCCOLLACTOR SOLUTION SOLU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;
                                                                                                                                        61 dspavngatghs-ssldarevipmaavkgalreagdefelryrrafsdltsglhitpgta 119
                                                                                                                                                                                                                                   yqsfeqvvnelfrdgvnwgrivaffsfggalcvesvdkemqvlvsriaawmatylndh-1 178
                                                                                                                                                                                                                                                         60 hhrpeppgsaaasevppae-glrpapp-g-vhlalrqagdefsrryqrdfaqmsgqlhlt 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44 QQEQEAEGVAAPADPEMVTLPLQPSSTMGQVGRQLAIIGDDINRRYDSEFQTMLQHLQPT 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 pftahgrfvavveelfrdgvnwgrivaffefggvmcvesvnremsplvdniatwmteyl🕩 176
                                                                                                                                                                  CAZALS-HATEM D.L., LOUIE D.C., TANAKA S., REED J.C.;
BIOCHIM. BIOPHYS. ACTA 1132:109-113(1992).
-!- FONCTION: PROLONGS THE SURVIVAL. OF HEWATOPOIETIC CELLS IN THE ABSENCE OF REQUIRED REWITH FACTORS AND ALSO IN THE PRESENCE OF VARIOUS STIMULI INDUCING CELLULAR DEATH. BLOCKS APOPTOSIS. MIGHT FUNCTION IN AN ANTIOXIDANT PATHWAY TO PREVENT APOPTOSIS AT SITES OF FREE MADICAL GENERATION SUCH AS MITOCHONDRIA.
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE
(BY SIMILARITY).
                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 245; DB 1; Length 233;
Pred. No. 4.70e-25;
40; Mismatches 57; Indels 6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
E -> S (IN REF. 2).
GSAAASEVPPAEGLRP -> ARLLLVRCPRLRGCA
                                                                                               4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!-TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES.
-!-SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
EMBL; D11382; G22794; -.
EMBL; D11381; G222794; JOINED.
EMBL; D11381; G222794; JOINED.
EMBL; D11961; G65970; -.
PIR; A37332; A37332.
PIR; S24390; S24390.
PROSITE; PS01080; BCL2.
APOPTOSIS; TRANSMEMBRARE; MITOCHONDRION.
TRANSMEM 208 228 POTENTIAL.
                                                  Length 233;
                                                                                             Indels
                                                                                           41; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (IN REF. 2).
H -> T (IN REF. 2).
G -> V (IN REF. 2).
4; 3376502C CRC32;
                                           16.1%; Score 250; DB 1;
larity 25.5%; Pred. No. 5.51e-26;
Conservative 41; Mismatches 60
26049 MW; 57C67491 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
APOPTOSIS REGULATOR BCL-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  233 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINES, 92375724.
BGUCHI Y., EWERT D.L., TSUJIMOTO Y.;
NUCLEIC ACIDS RES. 20:4187-4192(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                 || : ||| : ::| || :
167 ARWIAQRGGWVAALNL-GNGP 186
                                                                                                                                                                                                                                                                                                                         179 epwiqenggwdtfvelygnna 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                139 C
25687 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h 15.8%;
Similarity 28.5%;
41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
139
233 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
  233 AA;
                                                                Best Local Similarity
Matches 36; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 92379084.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GALLIFORMES.
                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 4
ID BCL2_CHICK
AC Q00709;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
SEQUENCE
                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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NATURE 348:334-336(1990).

-!- FUNCTION: PROLOMOS THE SURVIVAL OF HEMATOPOIETIC CELLS IN THE
ABSENCE OF REQUIRED GROWTH FACTORS AND ALSO IN THE PRESENCE OF
VARIOUS STIMULI INDUCING CELLULAR DEATH. BLOCKS APOPTOSIS. MIGHT
FUNCTION IN AN ANTIOXIDANT PARHWAY TO PREVENT APOPTOSIS. MIGHT
FUNCTION IN AN ANTIOXIDANT PARHWAY TO PREVENT APOPTOSIS AT SITES
OF FREE RADICAL GENERATION SUCH AS MITCCHONDRIA.

-!- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE.
-!- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES.
-!- DISEASE: INVOLVED IN FOLLICULAR LYMPHOMA (FL) (ALSO KNOWN AS TYPE
II CHRONIC LYMPHATIC LEUKEMIA) BY A CHROMOSOMAL TRANSLOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        132 tvveelfrdgvnwgrivaffefggvmcvesvnremsplvdnialwmteylnrh-lhtwig 190
74 tpaapgaaagpalspvppvvhlt--lrqagddfsrryrrdfaemssglhltpftargrfa 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- ALTERNATIVE PRODUCTS: TWO FORMS OF BCL-2: ALPHA, AND BETA, ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THEY ONLY DIFFER AT THEIR C-TENAINAL ENDS.
-1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
PMR1, M19395; G173369; ALT_SEQ.
PIR: B29409; TW1081.
PIR: D37332; D37332.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T(14;18)(032;021) WHICH INVOLVES BCL2 AND IMMUNOGLOBULIN GENE
                                                                                                                                                                                              HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS01080; BCL2.
PROTO-ONCOGENE; APOPTOSIS; ALTERNATIVE SPLICING; MEMBRANE; MITOCHONDRION; CHROMOSOMAL TRANSLOCATION.
SEQUENCE 205 AA; 22311 MW; ED321E5E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 15.4%; Score 239; DB 1; Length 205; Best Local Similarity 29.7%; Pred. No. 6.08e-24; Matches 38; Conservative 34; Mismatches 51; Indels
                                                                                                                                                                                                                                                                    TSUJIMOTO Y., CROCE C.M.;
PROC. NATL. ACAD. SCI. U.S.A. 83:5214-5218(1986).
                                                                                                                                 01-WAR-1989 (REL. 10, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
                                                                                                            205 AA
                                                                                                                                                                                                                                                                                                                                   EGUCHI Y., EWERT D.L., TSUJIMOTO Y.;
NUCLEIC ACIDS RES. 20:4187-4192(1992).
                                                                                                             PRT;
                                  177 rh-lhnwiqdnggwdafvelygns 199
                                                   :| : || : || | ::| ||:
163 HHCIARWIAQRGGWVAALNL-GNG 185
                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                            REVISIONS TO 96 AND 110.
                                                                                                                                                                                                                                                                                                                                                              [3]
SUBCELLULAR LOCATION.
                                                                                                                                                                       PROTEIN BCL-2-BETA.
                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE; 86259760.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        191 dnggwvga 198
                                                                                                                                                                                                                                                                                                                          MEDLINE; 92375724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172 QRGGWVAA 179
                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 91066924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIM; 151430;
                                                                                                 LT 5
BC2B_HUMAN
P10416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGIONS
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HOCKENBERY D., NUNEZ G., MILLIMAN C., SCHREIBER R.D., KORSMEYER S.J.;
NATURE 348:334-336(1990).

-!- FUNCTION: PROLONGS THE SURVIVAL OF HEMATOPOIETIC CELLS IN THE
ABSENCE OF REQUIRED GROWTH FACTORS AND ALSO IN THE PRESENCE OF
VARIOUS STIMULI INDOCINED GROWTH. BLOCKS APOPTOSIS. MIGHT
FUNCTION IN AN ANTIOXIDANT PATHWAY TO PREVENT APOPTOSIS AT SITES
OF FREE RADICAL GENERATION SUCH AS MITOCHONDRIA.
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE.
-!- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES.
-!- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES.
-!- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES.
-!- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES.
-!- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES.
-!- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES.
-!- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES.
-!- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES.
-!- TISSUES SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES.
-!- TISSUES SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES.
-!- TISSUES SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES.
-!- TISSUES SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES.
-!- TISSUES SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES.
-!- TISSUES SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES.
-!- TISSUES SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54 APADPEMVTLP-LQPSSTMGQVGRQLAIIGDDINRRYDSEFQTMLQHLQPTAENAYEYFT 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1-ALTERNATIVE PRODUCTS: TWO FORMS OF BCL-2: ALPHA, AND BETA, ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THEY ONLY DIFFER AT THEIR C-TERMINAL ENDS.
-1-SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
EMBL; M13994; G179367; ALT_SEQ.
EMBL; M14745; G179371; -...
PIR; A29409; TVHUBL.
PIR; A24428; TVHUBC.
PIR; C37332; C37332.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIM; 151430; -
PROSITE; PSO1080; BCL2.
PROSITE; PSO1080; BCL2.
PROTO-ONCOGENE; APOPTOSIS; ALTERNATIVE SPLICING; TRANSMEMBRANE;
MITOCHOUDRION; CHROMOSOMAL TRANSLOCATION.
TRANSMEM 213 POTENTIAL.
CONFLICT 59 59 P -> T (IN REF. 3).
CONFLICT 117 117 S -> R (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9;
                                                                                                                                                                                                                                                                HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 239; DB 1; Length 239;
Pred. No. 6.08e-24;
36; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROC. NATL. ACAD. SCI. U.S.A. 83:5214-5218(1986).
                                                                                                                                 LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                   239 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 92375724.
EGUCHI Y., EWERT D.L., TSUJIMOTO Y.;
NUCLEIC ACIDS RES. 20:4187-4192(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 87002488.
CLEARY M.L., SMITH S.D., SKLAR J.;
CELL 47:19-28(1986).
                                   PRT;
                                                                                              CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [2]
REVISIONS TO 96; 110 AND 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 29.3%;
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISUJIMOTO Y., CROCE C.M.;
                               STANDARD;
                                                                                       01-MAR-1989 (REL. 10,
01-APR-1993 (REL. 25,
01-NOV-1995 (REL. 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION.
                                                                                                                                                                                                PROTEIN BCL-2-ALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE; 86259760.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91066924
LT 6
BC2A_HUMAN
P10415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
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PRT;
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Local Similarity 27.2%;
nes 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 30.4%; 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEIN BCL-2 ALPHA.
BCL2 OR BCL-2.
RATTUS NORVEGICUS (RAT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EUTHERIA; RODENTIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-1996 (
01-0CT-1996 (
01-0CT-1996 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LT 9
BCL2_RAT
P49950;
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78 LAIIGDDINRRYDSEFQTMLQHLQPTAENAYEYFTKIATSLFESG-NWGRVVALLGFGYR 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CELL 49:455-463(1987).

-1- FUNCTION: PROLONGS THE SURVIVAL OF HEMATOPOIETIC CELLS IN THE ABSENCE OF ROLONGS GROWTH FACTORS AND ALSO IN THE PRESENCE OF VARIOUS STIMULI INDUCING CELLULAR DEATH. BLOCKS APOPTOSIS. MIGHT FUNCTION IN AN ANTIOXIDANT PATHWAY TO PREVENT APOPTOSIS. MIGHT FUNCTION IN AN ANTIOXIDANT PATHWAY TO PREVENT APOPTOSIS AT SITES OF FREE RADICAL GENERALION SUCH AS MITOCHONDRIA.
-1- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE.
-1- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES.
-1- ALTERNATIVE PRODUCTS: TWO FORMS OF BCL-2: ALDHA, AND BETA, ARE PRODUCED BY ALIERNATIVE SPLICING OF THE SAME GENE. THEY ONLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                     01-MAR-1989 (REL. 10, CREATED)
01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
PROTEIN BCL-2.
BCL2 OR BCL-2.
MUS MUSCULUS (MOUSE).
BUXARYOTA: METAROA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
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EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                      NEGRINI M., SILINI E., KOZAK C., TSUJIMOTO Y., CROCE C.M.; CELL 49:455-463(1987).
-1- FUNCTION: PROLONGS THE SURVIVAL OF HEMATOPOLETIC CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NEGRINI M., SILINI E., KOZAK C., TSUJIMOTO Y., CROCE C.M.; CELL 49:455-463(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 234; DB 1; Length 199;
Pred. No. 5.08e-23;
28; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DIFFER AT THEIR C-TERMINAL ENDS.
-1-SINILARITY: BALLONGS TO THE BCL-2 FAMILY.
EMBL; M16506; G387110; -.
PIR; B25960; TVMSB1.
PROSITE; PS01080; BCL2
APOPTOSIS; ALTERNATIVE SPLICING; MEMBRANE; MITOCHONDRION.
SEQUENCE 199 AA; 12299 MW; 3E60FA47 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       154 mcvesvnremsplvdnialwmteylnrh-lhtwiqdnggwvga 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137 LALHVYQHGLTGFLGQVTRFVVDFMLHHCIARWIAORGGWVAA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-1989 (REL. 10, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
10-CTT-1996 (REL. 34, LAST ANNOTATION UPDATE)
PROTEIN BCL-2 ALPHA.
                                                                                                                                                199 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REVISIONS TO 221-222.
MEDLINE; 92375724.
EGUCHI Y., EWERT D.L., TSUJIMOTO Y.;
                                                                                                                                                   PRT;
                                       172 QRGGWVAALNIGNGPILNVL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-LIVER;
MEDLINE; 87187643.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Guery Match
Best Local Similarity 31.18;
                191 dnggwdafvel-ygpsmrpl
                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                 EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE; 87187643.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BCL2 OR BCL-2.
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P10417;
                                                                                                                                                BC2B_MOUSE
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NUCLEIC ACIDS RES. 20:4187-4192(1992).

"INUCLEIC ACIDS RES. 20:4187-4192(1992).

"INUCLEIC ACIDS RES. 20:4187-4192(1992).

"EABENCE OF REQUIRED GROWTH PACTORS AND ALSO IN THE PRESENCE OF PRESENCE OF REQUIRED CROWTH PACTORS AND ALSO IN THE PRESENCE OF RECEDIAL INDICING CELLULAR DEATH. BLOCKS APOPTOSIS. MIGHT FUNCTION IN AN ANTIOXIDANT PATHARY TO PREVENT APOPTOSIS AT SITES OF FREE RADICAL GENERATION SUCH AS MITOCHONDRIA.

"ILSUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE.

"ILSUBCELLULAR C-TERMIAL ENDS.

"ISTANDAL BALOMED BY ALTERNATIVE SPLICING. THE SAME GENE. THEY ONLY DIFFER AT THEIR C-TERMIAL ENDS.

"EMBL. 13152; G387109; ".

"EMBL. 13152; G387109; ".

"EMBL. MITOCHONDRION.

"PROSTITE: PSO1000; BGLZ.

"ROPIOSIS; ALTERNATIVE SPLICING; TRANSMEMBRANE; MITOCHONDRION.

"PROSTITE: PSO1000; BGLZ.

"PROSTITE: PSO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 rdtaartsplrp-lvanagpalspvppvvhltlrragddfsrryrrdfaemssglhltgf 121
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-!- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE.

-!- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES (BY
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SATO T., IRIE S., KRAJEWSKI S., REED J.C.;
GENE 140:291-292(1994).
-!- FUNCTION: PROLONGS THE SURVIVAL OF HEMATOPOIETIC CELLS IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      154 mcvesvnremsplvdnialwmteylnrh-lhtwiqdnggwdafvel-ygpsmrpl 206
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-!- ALTERNATIVE PRODUCIS: TWO FORMS OF BCL-2: ALPHA, AND BETA, AI
PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THEY ONLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DIFFER AT THEIR C-TERMINAL ENDS.
--- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
EMBL; L14680, G408947; --
TRADSPOSIS; ALTERNATIVE SPLICING; TRANSMEMBRANE; MITOCHONDRION.
TRANSMEM. 209 230 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŝ
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Pred. No. 1.18e-22;
42; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 234; DB 1; Length 236
Pred. No. 5.08e-23;
30; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  209 230 POTENTIAL.
236 AA; 26425 MW; 7ADFE975 CRC32;
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(REL. 34, LAST SEQUENCE UPDATE)
(REL. 34, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
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90 e-vff-rvaadmfsdgnfnwgrvvalfyfasklvlkalctkvpelirtimgwtldf-lre 146
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                                                                                                                                                                                                                                                                                   -!- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2.
-!- SUBCELLULAR LOCATION: MEMBRANE.
-!- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE CYTOPLASHIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY ALTERNATIVE SPLICING.
-!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
EMBL; L22473; G388166; --
BIR; A47538. A47538.
MIM; 600040; --
                                                                                           OLTVAI Z.N., MILLIMAN C.L., KORSMEYER S.J.;
CELL 74:609-619(19193).
-1- FUNCTION: ACCELERAFES PROGRAMMED CELL DEATH BY BINDING TO THE
APOPTOSIS REPRESSOR BCL-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 12.5%; Score 194; DB 1; Length 192
Local Similarity 24.5%; Pred. No. 7.87e-16;
Nes 40; Conservative 44; Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           147 rllgwiqdqggwdgllsyfgtptwqtvtifvagvltasltiwk 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APOPTOSIS; TRANSMEMBRANE; ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS01080; BCL2
                                                   MEDLINE; 93364978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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     셤
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nmelgrmladvdtdspre-vff-rvaadmfadgnfnwgrvvalfyfasklvlkalctkvp 130
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                                                                                                                                              targrfatvveelfrdgvnwgrivaffefggvmcvgsvnremsplvdnialwmteylnrh 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CELL 74:609-619(1993).
-!- FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO THE APOPTOSIS REPRESSOR BCL-2.
-!- ALTERNATIVE PRODUCTS: A 21 KD MEMBRANE PROTEIN ALPHA AND THE TWO CYTOPLASMIC PROTEINS BETA AND GAMMA ARE GENERATED BY ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :|:::: | : |: | | ||:: | | ||:: | |||::: | |||::: | ||::: | | ||::: | ||::: | ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||:: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||:: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||:: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||:: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||:: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||:: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||:: ||::: ||:: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||:: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||:::: ||::: ||::: ||::: ||::: ||:: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||:
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-1- SUBCELLUIAR LOCATION: MEMBRANE.
-1- SUBLIATY: BELONGS TO THE BCL-2 FAMILY.
-1- STAILARTY: BELONGS TO THE BCL-2 FAMILY.
-1- STAILARTY: BSLONGS TO THE BCL-3 FAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 206; DB 1; Length 192;
Pred. No. 5.98e-18;
49; Mismatches 75; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
APOPTOSIS REGULATOR BAX, MEMBRANE ISOFORM ALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   192 AA; 21394 MW; BD035304 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              192 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                                                                                                            182 -lhtwigdnggwdafvel-ygpsmrpl 206
: || : || || :| || :| |
165 CIARWIAQRGGWVAALNLGNGPILNVL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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Best Local Similarity 25.6%;
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-C57BL/6 X DBA/2 F1;
MEDLINE; 93364978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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Q07813;
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Q07812;
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Length 192;

172 192 POTENTIAL. 192 AA; 21184 MW; B2E6148A CRC32;

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                                                                                                                                                                                                                                                                               -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
-1- SUBCELLULAR LOCATION: CYTOPLASMIC.
-1- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY ALTERNATIVE SPLICING.
-1- SIMILARTY: BELONGS TO THE BCL-2 FAMILY.
-1- SIMILARTY: BLONGS TO THE BCL-2 FAMILY.
-1- PIR: B47538: B47538.
                                                                                                                                                                                                                                                      -!- FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO THE APOPTOSIS REPRESSOR BCL-2.
                                                                                                                           EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 189; DB 1; Length 218
Pred. No. 5.86e-15;
35; Mismatches 58; Indels
             Q07814;
01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-CCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
APOPTOSIS REGULATOR BAX, CYTOPLASMIC ISOFORM BETA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               82B2FF09 CRC32;
                                                                                                                                                                                           TISSUE=B-CELL;
MEDLINE; 93364978.
OLTVAL Z.N., MILLIMAN C.L., KORSMEYER S.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS01080; BCL2.
APOPTOSIS; ALTERNATIVE SPLICING.
SEQUENCE 218 AA; 24220 MW; 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 12.2%;
Best Local Similarity 27.0%;
Matches 37; Conservative
 STANDARD;
                                                                                                                                                                                                                                        CELL 74:609-619(1993).
                                                                                                              HOMO SAPIENS (HUMAN)
                                                                                                                                           EUTHERIA; PRIMATES.
                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                    MIM; 600040;
BAXB_HUMAN
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HOMO SAPIENS (HUMAN). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; PRIMATES.

SEQUENCE FROM N.A.

01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
APOPTOSIS REGULATOR BAX, MEMBRANE ISOFORM ALPHA.

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EUTHERIA; PRIMATES
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HSA1_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PROBABLE).
-!- INDUCTION: EXPRESSION INCREASES EARLY DURING PHORBOL-ESTER INDUCED DIFFERENTIATION ALONG THE MONOCYTE/MAGROPHAGE PATHWAY IN WYELOID LEGKEMIA CELL LINES MIL.
-!- SIMILARITY: BELONGS TO THE BCL2 FAMILY.
EMBL: L08246: -; NOT_ANNOTATED_CDS.
PIN: 129552; --
PROSITE: PSO1080: BCL2
APOPTOSIS; TRANSMEMBRANE; DIFFERENTIATION.
ONSURE 227 OR A.
                       0-vff-rvaadmfsdgnfnwgrvvalfyfasklvlkalctkvpelirtimgwtldf-lre 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        174 lyrqsleiisrylreqatgakdtkpmgrsgatsrkaletlrrygdgygrnhetvfggmlr 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    234 kldikneddvkslsrvmihvfsdgvtnwgrivtlisfgafvakhlktingescieplaes 293
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MEDILNE; 93.34.28.
PROC. NATL. ACAD. ST. U.S.A. 90:3516-3520(1993).
-I- FUNCTION: INVOLVED IN PROGRAMMING OF DIFFERENTIATION AND
CONCOMITANT MAINTENANCE OF VIABILITY BUT NOT OF PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               baa.
Homo Sapiens (Human).
Eukaryota; metazoa; Chordata; Vertebrata; Tetrapoda; mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                           HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                               MCLI_HUMAN STANDARD; PRT; 350 AA.
007830;
01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
INDUCED MYELOID LEUKEMIA CELL DIFFERENTIATION PROTEIN MCLI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 176; DB 6; Length 350;
Pred. No. 1.00e-12;
39; Mismatches 63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OR A. POTENTIAL. 10194B64 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P55269;
01-0CT-1996 (REL. 34, CREATED)
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
BAX PROTEIN, CYTOPLASMIC ISOFORM DELTA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUE-MYELOID LEUKEMIA CELLS;
MEDLINE; 93234528.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                330 349 P
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Best Local Similarity 24.3%;
Matches 34; Conservative
                                                                                                                                                            147 rllgwigdgggwyrllk 163
                                                                                                                                                                                                   165 CIARWIAQRGGWVAALN 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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BAXD_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -:- SÜBCELLULAR LOCATION: INTRACELLULAR.
-:- TISSUE SPECIFICITY: EXPRESSED IN HEMOPOIETIC TISSUES, INCLUDING
BONE MARROW SPLEEN AND THYMUS.
-:- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
EMBL: 116462; G293274; -..
APOPTOSIE; PS01080; BCL2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                        88 rivtifafggvllkklpqeqialdvcaykqvssfvaefimnn-tgewirqnggw 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                      Length 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 172;
                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
HEMOPOIETIC-SPECIFIC EARLY RESPONSE PROTEIN (A1 PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46; Indels
                                                                                                                                                                                                                                                                                                                                                                 95 lrerllgwigdaggwdgllsyfgtptwqtvtifvagvltasltiwk 140
                                                                                                                                                                                                                                                                                                                                                                                         43;
                                                                                                                                                                                                                                   10.6%; Score 165; DB 1; 127.4%; Pred. No. 7.08e-11; ative 30; Mismatches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 10.2%; Score 158; DB 5; I Local Similarity 28.1%; Pred. No. 1.01e-09; Nes 32; Conservative 29; Mismatches 46;
                                                                                                                                                                               APOPTOSIS; ALTERNATIVE SPLICING.
SEQUENCE 143 AA; 15772 MW; 71AA1CBD CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN 24 33 ALA/PRO-RICH.
SEQUENCE 172 AA; 19914 MW; FFD38D6F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      172 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                  larity 27.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MUS MUSCULUS (MOUSE)
                                                                                                                                                                                                                                                 t Local Similarity
ches 29; Conser
SEQUENCE FROM N.A. MEDLINE; 95331797.
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Search completed: Wed Aug 20 11:14:06 1997 Job time : 26 secs.

